

OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:32 ; Search time 50.5 Seconds  
(without alignments)  
44.760 Million cell updates/sec

Title: US-09-668-314C-70  
Perfect score: 8  
Sequence: 1 EVKMDAEF 8

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	100.0	8	3	AAy94772	Beta-secr
2	8	100.0	8	4	AAU07230	Human bet
3	8	100.0	8	4	AAE10660	Human Asp
4	8	100.0	8	4	AAE06902	Human amy
5	8	100.0	8	4	AAE02612	Human Asp
6	8	100.0	8	4	AAU06635	Synthetic
7	8	100.0	8	4	AAU06631	Beta secr
8	8	100.0	8	5	ABB78621	APP Swedi
9	8	100.0	9	2	AAW82083	Fluorogen

10	8	100.0	9	3	AAy87949
11	8	100.0	9	3	AAB07873
12	8	100.0	9	5	ABU60430
13	8	100.0	9	7	ADC26556
14	8	100.0	10	2	AAR22054
15	8	100.0	10	2	AAR24261
16	8	100.0	10	2	AAW82440
17	8	100.0	10	3	AAy69703
18	8	100.0	10	4	AAU07227
19	8	100.0	10	4	AAE10654
20	8	100.0	10	4	AAE06899
21	8	100.0	10	4	AAB46208
22	8	100.0	10	4	AAB46207
23	8	100.0	10	4	AAB46209
24	8	100.0	10	4	AAB61336
25	8	100.0	10	4	AAE02606
26	8	100.0	10	4	AAB66574
27	8	100.0	10	4	AAG62668
28	8	100.0	10	4	AAU06628
29	8	100.0	10	5	ABB06426
30	8	100.0	10	5	ABG78375
31	8	100.0	10	5	ABB78615
32	8	100.0	10	5	AAU99490
33	8	100.0	10	5	ABG30940
34	8	100.0	10	6	ABG76103
35	8	100.0	10	6	ABR61933
36	8	100.0	10	6	ADA74819
37	8	100.0	10	7	ADB75175
38	8	100.0	11	4	AAB97468
39	8	100.0	11	4	AAB75144
40	8	100.0	11	4	AAB75143
41	8	100.0	12	4	AAB74931
42	8	100.0	12	5	ABB08997
43	8	100.0	12	5	AAE16657
44	8	100.0	12	5	AAU74831
45	8	100.0	12	5	ABB07592
46	8	100.0	12	6	ABP97969
47	8	100.0	12	6	AAO26795
48	8	100.0	12	7	ADC29717
49	8	100.0	12	7	ADD80763
50	8	100.0	13	2	AAW70869
51	8	100.0	13	5	AAM50891
52	8	100.0	13	6	ABP57078
53	8	100.0	13	6	ABP71462
54	8	100.0	13	6	AAO16443
55	8	100.0	13	6	ABP71263
56	8	100.0	13	6	ABR44371
57	8	100.0	13	6	ABP58369
58	8	100.0	13	6	ABG75934
59	8	100.0	13	6	ABP71624
60	8	100.0	13	6	AAE35994
61	8	100.0	13	6	ABR42269
62	8	100.0	13	6	ABR82366
63	8	100.0	13	6	ABR56252
64	8	100.0	13	6	ABR62012
65	8	100.0	13	6	ABR61881
66	8	100.0	13	7	ADB75166

Aay87949	Mammalian
Aab07873	A peptide
Abu60430	Protease
Adc26556	Beta-secr
Aar22054	Peptide P
Aar24261	Human amy
Aaw82440	Human amy
Aay69703	Beta-APP
Aau07227	Human bet
Aae10654	Human wil
Aae06899	Human amy
Aab46208	Human APP
Aab46207	Human APP
Aab46209	Human APP
Aab61336	Sythetic
Aae02606	Human wil
Aab66574	Synthetic
Aag62668	Beta-shee
Aau06628	Asp2 reco
Abb06426	Human APP
Abg78375	Human bet
Abb78615	Beta-secr
Aau99490	Peptide #
Abg30940	Nogo/BACE
Abg76103	Amyloid p
Abr61933	Human APP
Ada74819	Human amy
Adb75175	Amyloid b
Aab97468	Asp2 subs
Aab75144	Asp 1 sub
Aab75143	APP beta-
Aab74931	Beta-amyl
Abb08997	Amyloid p
Aae16657	APP subst
Aau74831	Synthetic
Abb07592	Biotinylna
Abp97969	A synthet
Aao26795	Beta-secr
Adc29717	Synthetic
Add80763	Synthetic
Aaw70869	Beta-amyl
Aam50891	Fluoresce
Abp57078	Synthetic
Abp71462	Beta-secr
Aao16443	Beta-secr
Abp71263	Synthetic
Abr44371	Synthetic
Abp58369	Synthetic
Abg75934	Synthetic
Abp71624	Beta-secr
Aae35994	APP subst
Abr42269	Amyloid p
Abr82366	Synthetic
Abr56252	Amyloid P
Abr62012	Amino aci
Abr61881	Beta-secr
Adb75166	Human amy

67	8	100.0	13	7	ABR56173	Abr56173	Amyloid p
68	8	100.0	13	7	ADC10525	Adc10525	Synthetic
69	8	100.0	15	4	AAU07234	Aau07234	Human bet
70	8	100.0	15	4	AAE10669	Aae10669	Quenched
71	8	100.0	15	4	AAE06906	Aae06906	Human Asp
72	8	100.0	16	3	AAB06315	Aab06315	Human bet
73	8	100.0	16	3	AAB06317	Aab06317	Human bet
74	8	100.0	18	4	AAE00608	Aae00608	Beta-amyl
75	8	100.0	19	2	AAR14135	Aar14135	Brain-der
76	8	100.0	20	3	AAV69713	Aay69713	Beta-APP
77	8	100.0	21	2	AAW82188	Aaw82188	Fluorogen
78	8	100.0	21	4	AAG73206	Aag73206	Protease
79	8	100.0	23	4	AAB97473	Aab97473	Asp2 subs
80	8	100.0	23	4	AAB75147	Aab75147	Asp 1 sub
81	8	100.0	33	2	AAW98002	Aaw98002	Amyloid p
82	8	100.0	39	3	AAV69717	Aay69717	Beta-APP
83	8	100.0	45	2	AAW26392	Aaw26392	Amyloid p
84	8	100.0	45	2	AAW26512	Aaw26512	Amyloid p
85	8	100.0	45	2	AAW42977	Aaw42977	Deletion
86	8	100.0	45	2	AAW44748	Aaw44748	APP-REP 7
87	8	100.0	52	6	ABP97925	Abp97925	Amino aci
88	8	100.0	52	6	ABP97924	Abp97924	Amino aci
89	8	100.0	52	6	ADA90299	Ada90299	Abeta ami
90	8	100.0	53	2	AAR55695	Aar55695	Sequence
91	8	100.0	53	2	AAR55697	Aar55697	Sequence
92	8	100.0	53	2	AAR55696	Aar55696	Sequence
93	8	100.0	53	2	AAR64168	Aar64168	Variant b
94	8	100.0	54	3	AAB32126	Aab32126	Amyloid-b
95	8	100.0	57	3	AAB10910	Aab10910	Human amy
96	8	100.0	58	2	AAR58937	Aar58937	Amyloid p
97	8	100.0	59	2	AAW05375	Aaw05375	Amyloid p
98	8	100.0	59	2	AAW70863	Aaw70863	Beta-amyl
99	8	100.0	59	4	AAB84425	Aab84425	Partial s
100	8	100.0	59	7	ADB75160	Adb75160	Human bet
101	8	100.0	60	3	AAV69701	Aay69701	Beta-amyl
102	8	100.0	63	2	AAW26391	Aaw26391	Amyloid p
103	8	100.0	63	2	AAW26511	Aaw26511	Amyloid p
104	8	100.0	63	2	AAW42976	Aaw42976	Beta-amyl
105	8	100.0	63	2	AAW42975	Aaw42975	Beta-amyl
106	8	100.0	63	2	AAW44746	Aaw44746	APP-REP 7
107	8	100.0	63	2	AAW44747	Aaw44747	APP-REP 7
108	8	100.0	63	7	ADB33534	Adb33534	APP regio
109	8	100.0	63	7	ADB33537	Adb33537	APP regio
110	8	100.0	64	5	ABB81320	Abb81320	Amyloid p
111	8	100.0	67	2	AAW71377	Aaw71377	Peptide d
112	8	100.0	82	5	AAU80960	Aau80960	Human amy
113	8	100.0	82	5	ABG94280	Abg94280	Amyloid b
114	8	100.0	82	5	ABG80592	Abg80592	Human amy
115	8	100.0	93	4	ABG19083	Abg19083	Novel hum
116	8	100.0	103	2	AAR74697	Aar74697	Beta-amyl
117	8	100.0	103	2	AAW51317	Aaw51317	Natural b
118	8	100.0	103	2	AAW89372	Aaw89372	Beta-amyl
119	8	100.0	103	3	AAV56103	Aay56103	Beta amyl
120	8	100.0	103	4	AAE12509	Aae12509	Beta-amyl
121	8	100.0	103	5	ABG71002	Abg71002	Amyloid p
122	8	100.0	103	5	ABB05150	Abb05150	Beta amyl
123	8	100.0	103	6	ABG73457	Abg73457	Amyloid p

124	8	100.0	104	2	AAW51100	Aaw51100	Amino aci
125	8	100.0	112	2	AAR93556	Aar93556	Familial
126	8	100.0	115	2	AAW97999	Aaw97999	London-FA
127	8	100.0	117	2	AAW51102	Aaw51102	Flag-amyl
128	8	100.0	162	1	AAP83151	Aap83151	Deduced s
129	8	100.0	162	2	AAR10023	Aar10023	Beta-amyl
130	8	100.0	162	2	AAR37863	Aar37863	Deduced f
131	8	100.0	249	2	AAR65798	Aar65798	Beta-amyl
132	8	100.0	264	1	AAP90609	Aap90609	Sequence
133	8	100.0	264	1	AAP90497	Aap90497	Protein s
134	8	100.0	416	5	ABB81212	Abb81212	Human amy
135	8	100.0	487	2	AAW26394	Aaw26394	Amyloid p
136	8	100.0	487	2	AAW26510	Aaw26510	Amyloid p
137	8	100.0	487	2	AAW42979	Aaw42979	Amyloid p
138	8	100.0	487	2	AAW44745	Aaw44745	APP-REP 7
139	8	100.0	492	2	AAR45229	Aar45229	APP-REP 7
140	8	100.0	492	2	AAW26393	Aaw26393	Amyloid p
141	8	100.0	492	2	AAW26509	Aaw26509	Amyloid p
142	8	100.0	492	2	AAW42978	Aaw42978	Amyloid p
143	8	100.0	492	2	AAW44744	Aaw44744	APP-REP 7
144	8	100.0	534	6	ABB99605	Abb99605	Amino aci
145	8	100.0	537	2	AAR40114	Aar40114	APP-HCV-E
146	8	100.0	596	2	AAR65797	Aar65797	Beta-amyl
147	8	100.0	627	3	AAB10955	Aab10955	SEAP/huma
148	8	100.0	651	2	AAR65796	Aar65796	Beta-amyl
149	8	100.0	656	2	AAR58935	Aar58935	Amyloid p
150	8	100.0	670	2	AAR65795	Aar65795	APP751 be
151	8	100.0	676	2	AAR58936	Aar58936	Amyloid p
152	8	100.0	695	1	AAP81692	Aap81692	Sequence
153	8	100.0	695	2	AAR05166	Aar05166	Sequence
154	8	100.0	695	2	AAR14046	Aar14046	Amyloid p
155	8	100.0	695	2	AAR26338	Aar26338	APP695. 3
156	8	100.0	695	2	AAR58923	Aar58923	Mouse amy
157	8	100.0	695	2	AAR58920	Aar58920	Amyloid p
158	8	100.0	695	2	AAW19481	Aaw19481	APP695 mu
159	8	100.0	695	2	AAW19484	Aaw19484	APP695 mu
160	8	100.0	695	2	AAW19498	Aaw19498	APP695 mu
161	8	100.0	695	2	AAW19495	Aaw19495	APP695 mu
162	8	100.0	695	2	AAW20233	Aay20233	Human bet
163	8	100.0	695	2	AAW49690	Aay49690	Human bet
164	8	100.0	695	2	AAW07221	Aay07221	Amyloid p
165	8	100.0	695	3	AAW88434	Aay88434	Human APP
166	8	100.0	695	3	AAW88436	Aay88436	Human APP
167	8	100.0	695	3	AAW44705	Aay44705	Human bet
168	8	100.0	695	4	AAU07207	Aau07207	Human bet
169	8	100.0	695	4	AAE10632	Aae10632	Human wil
170	8	100.0	695	4	AAE10634	Aae10634	Human amy
171	8	100.0	695	4	AAE06864	Aae06864	Human amy
172	8	100.0	695	4	AAE06862	Aae06862	Human wil
173	8	100.0	695	4	AAE02584	Aae02584	Human amy
174	8	100.0	695	4	AAE02586	Aae02586	Human amy
175	8	100.0	695	4	AAE03420	Aae03420	Human amy
176	8	100.0	695	4	AAU06608	Aau06608	Human Amy
177	8	100.0	695	4	AAU06606	Aau06606	Human Amy
178	8	100.0	695	5	ABB78595	Abb78595	Human APP
179	8	100.0	695	5	ABB78593	Abb78593	Human APP
180	8	100.0	695	5	AAG68315	Aag68315	Human amy



181	8	100.0	695	5	ABG32721	Abg32721	Human	amy
182	8	100.0	695	6	ABP97918	Abp97918	Amino	aci
183	8	100.0	695	6	ABB99604	Abb99604	Amino	aci
184	8	100.0	695	7	ADB87311	Adb87311	Human	amy
185	8	100.0	695	7	ADB33519	Adb33519	Human	APP
186	8	100.0	695	7	ADC65997	Adc65997	Human	APP
187	8	100.0	697	3	AAy88430	Aay88430	Human	APP
188	8	100.0	697	3	AAy88428	Aay88428	Human	APP
189	8	100.0	697	4	AAU07208	Aau07208	Human	bet
190	8	100.0	697	4	AAU07210	Aau07210	Human	bet
191	8	100.0	697	4	AAE10635	Aae10635	Human	amy
192	8	100.0	697	4	AAE10637	Aae10637	Human	amy
193	8	100.0	697	4	AAE06867	Aae06867	Human	amy
194	8	100.0	697	4	AAE06865	Aae06865	Human	amy
195	8	100.0	697	4	AAE02589	Aae02589	Human	amy
196	8	100.0	697	4	AAE02587	Aae02587	Human	amy
197	8	100.0	697	4	AAU06609	Aau06609	Human	Amy
198	8	100.0	697	4	AAU06611	Aau06611	Human	Amy
199	8	100.0	697	5	ABB78596	Abb78596	Human	APP
200	8	100.0	697	5	ABB78598	Abb78598	Human	APP
201	8	100.0	733	6	ABR43271	Abr43271	Human	neu
202	8	100.0	740	7	ADB87314	Adb87314	Human	amy
203	8	100.0	740	7	ADB87312	Adb87312	Human	amy
204	8	100.0	751	1	AAP83150	Aap83150	Amino	aci
205	8	100.0	751	1	AAP94776	Aap94776	Novel	amy
206	8	100.0	751	2	AAR05718	Aar05718	NAP-2	gen
207	8	100.0	751	2	AAR10022	Aar10022	Beta-amy	l
208	8	100.0	751	2	AAR20328	Aar20328	Sequence	
209	8	100.0	751	2	AAR37862	Aar37862	Beta-amy	l
210	8	100.0	751	2	AAW19486	Aaw19486	APP751	mu
211	8	100.0	751	2	AAW19483	Aaw19483	APP751	mu
212	8	100.0	751	2	AAW19496	Aaw19496	APP751	mu
213	8	100.0	751	2	AAW19499	Aaw19499	APP751	mu
214	8	100.0	751	2	AAy08615	Aay08615	Human	bet
215	8	100.0	751	2	AAy08605	Aay08605	Human	bet
216	8	100.0	751	4	AAE10649	Aae10649	Human	amy
217	8	100.0	751	4	AAE06894	Aae06894	Human	amy
218	8	100.0	751	4	AAE02601	Aae02601	Human	amy
219	8	100.0	751	4	AAU06623	Aau06623	Human	par
220	8	100.0	751	5	ABB78610	Abb78610	Human	APP
221	8	100.0	751	5	AAG68316	Aag68316	Human	amy
222	8	100.0	751	5	ABG32722	Abg32722	Human	amy
223	8	100.0	751	5	AAO18050	Aao18050	Amyloid	p
224	8	100.0	753	4	AAU07224	Aau07224	Human	bet
225	8	100.0	753	4	AAE10651	Aae10651	Human	amy
226	8	100.0	753	4	AAE06896	Aae06896	Human	amy
227	8	100.0	753	4	AAE02603	Aae02603	Human	amy
228	8	100.0	753	4	AAU06625	Aau06625	Human	Amy
229	8	100.0	753	5	ABB78612	Abb78612	Human	APP
230	8	100.0	754	2	AAR26339	Aar26339	APP751.	3
231	8	100.0	754	2	AAW96210	Aaw96210	Amyloid	p
232	8	100.0	768	5	AAU80959	Aau80959	Human	amy
233	8	100.0	770	1	AAP94775	Aap94775	Novel	amy
234	8	100.0	770	2	AAR05717	Aar05717	NAP	gene
235	8	100.0	770	2	AAR26340	Aar26340	APP770.	3
236	8	100.0	770	2	AAR41546	Aar41546	Mutated	A
237	8	100.0	770	2	AAR63442	Aar63442	Amyloid	p

238	8	100.0	770	2	AAR62505	Aar62505	Amyloid p
239	8	100.0	770	2	AAW19485	Aaw19485	APP770 mu
240	8	100.0	770	2	AAW19482	Aaw19482	APP770 mu
241	8	100.0	770	2	AAW19497	Aaw19497	APP770 mu
242	8	100.0	770	2	AAW19500	Aaw19500	APP770 mu
243	8	100.0	770	2	AAW40130	Aaw40130	Human APP
244	8	100.0	770	2	AAW97996	Aaw97996	Human amy
245	8	100.0	770	4	AAE11762	Aae11762	Human amy
246	8	100.0	770	4	AAE10648	Aae10648	Human amy
247	8	100.0	770	4	AAE06913	Aae06913	Human amy
248	8	100.0	770	4	AAE06893	Aae06893	Human amy
249	8	100.0	770	4	AAE02600	Aae02600	Human amy
250	8	100.0	770	4	AAU06622	Aau06622	Human par
251	8	100.0	770	5	ABG94279	Abg94279	Amyloid b
252	8	100.0	770	5	ABB78609	Abb78609	Human APP
253	8	100.0	770	5	ABG76936	Abg76936	Humanised
254	8	100.0	770	5	AAG68317	Aag68317	Human amy
255	8	100.0	770	5	ABB78008	Abb78008	Amino aci
256	8	100.0	770	5	ABG80591	Abg80591	Human amy
257	8	100.0	770	5	ABG32723	Abg32723	Human amy
258	8	100.0	770	6	ABP72693	Abp72693	Human amy
259	8	100.0	770	6	ABR43902	Abr43902	Beta-amyl
260	8	100.0	770	6	ABP97885	Abp97885	Amino aci
261	8	100.0	770	6	ABR61931	Abr61931	Human amy
262	8	100.0	772	4	AAU07223	Aau07223	Human bet
263	8	100.0	772	4	AAE10650	Aae10650	Human amy
264	8	100.0	772	4	AAE06895	Aae06895	Human amy
265	8	100.0	772	4	AAE02602	Aae02602	Human amy
266	8	100.0	772	4	AAU06624	Aau06624	Human Amy
267	8	100.0	772	4	ABG19086	Abg19086	Novel hum
268	8	100.0	772	5	ABB78611	Abb78611	Human APP
269	8	100.0	777	4	ABG19089	Abg19089	Novel hum
270	8	100.0	783	7	ADB33513	Adb33513	Human APP
271	8	100.0	783	7	ADB33505	Adb33505	Human APP
272	8	100.0	798	4	ABG19088	Abg19088	Novel hum
273	8	100.0	941	7	ADB33509	Adb33509	Human APP
274	8	100.0	941	7	ADB33517	Adb33517	Human APP
275	8	100.0	1024	5	AAU75873	Aau75873	APP-LacI
276	7	87.5	7	5	AAE19124	Aae19124	Beta-secr
277	7	87.5	7	6	ABG75988	Abg75988	Amyloid p
278	7	87.5	9	7	ADE36577	Ade36577	APP epito
279	7	87.5	10	4	AAB46210	Aab46210	Human APP
280	7	87.5	10	4	AAB46206	Aab46206	Human APP
281	7	87.5	18	2	AAR75696	Aar75696	Unspecifi
282	7	87.5	32	2	AAW04400	Aaw04400	Mouse amy
283	7	87.5	48	4	AAB37523	Aab37523	Amyloid p
284	6	75.0	6	5	AAU78525	Aau78525	Beta amyl
285	6	75.0	10	4	AAB46211	Aab46211	Human APP
286	6	75.0	10	4	AAB46205	Aab46205	Human APP
287	6	75.0	50	4	AAG65957	Aag65957	Human A4
288	6	75.0	70	4	AAE09373	Aae09373	Human wil
289	6	75.0	70	4	AAU05015	Aau05015	Human amy
290	5	62.5	5	2	AAR37864	Aar37864	Beta-amyl
291	5	62.5	5	2	AAW08216	Aaw08216	Wild type
292	5	62.5	5	2	AAW61150	Aaw61150	Wild-type
293	5	62.5	5	2	AAU08608	Aay08608	Human NSE
294	5	62.5	5	2	AAU33750	Aay33750	Wild type

295	5	62.5	5	4	AAB47260
296	5	62.5	5	5	ABB06579
297	5	62.5	5	5	ABB06534
298	5	62.5	8	2	AAR42401
299	5	62.5	9	2	AAW82084
300	5	62.5	9	5	ABU60431
301	5	62.5	10	2	AAR24262
302	5	62.5	10	2	AAR24266
303	5	62.5	10	3	AAY69704
304	5	62.5	10	3	AAY69708
305	5	62.5	10	4	AAB46212
306	5	62.5	10	7	ADC26572
307	5	62.5	14	7	ADC99878
308	5	62.5	15	2	AAW05384
309	5	62.5	20	3	AAY69716
310	5	62.5	21	2	AAW82189
311	5	62.5	21	2	AAY30942
312	5	62.5	21	4	AAG73207
313	5	62.5	43	1	AAP96371
314	5	62.5	51	2	AAW53984
315	5	62.5	53	3	AAY87944
316	5	62.5	53	6	ABU08708
317	5	62.5	53	7	ADB61450
318	5	62.5	58	4	ABB39754
319	5	62.5	58	4	AAM33336
320	5	62.5	58	4	AAM73119
321	5	62.5	58	4	AAM60474
322	5	62.5	58	4	ABG54835
323	5	62.5	58	5	ABG42965
324	5	62.5	71	5	AAU72571
325	5	62.5	79	2	AAW53981
326	5	62.5	81	3	AAY99757
327	5	62.5	90	3	AAG47531
328	5	62.5	92	4	AAM96144
329	5	62.5	92	4	AAU22838
330	5	62.5	93	5	AAU72561
331	5	62.5	100	2	AAR10024
332	5	62.5	100	2	AAR37866
333	5	62.5	100	3	AAB13015
334	5	62.5	100	5	AAE14377
335	5	62.5	100	5	AAE14376
336	5	62.5	100	5	AAE14372
337	5	62.5	100	5	AAE14373
338	5	62.5	100	5	AAE14375
339	5	62.5	100	5	AAE14371
340	5	62.5	100	5	AAE14374
341	5	62.5	100	6	ABP97921
342	5	62.5	108	5	AAE14382
343	5	62.5	108	5	AAE14383
344	5	62.5	108	5	AAE14384
345	5	62.5	108	5	AAE14385
346	5	62.5	108	5	AAE14379
347	5	62.5	108	5	AAE14380
348	5	62.5	108	5	AAE14381
349	5	62.5	108	6	ABP97923
350	5	62.5	117	3	AAG55580
351	5	62.5	124	3	AAG47471

Aab47260	Wild type
Abb06579	Amyloid p
Abb06534	Beta-secr
Aar42401	Peptide r
Aaw82084	Fluorogen
Abu60431	Protease
Aar24262	Human amy
Aar24266	Human amy
Aay69704	Beta-APP
Aay69708	Beta-APP
Aab46212	Human APP
Adc26572	Beta-secr
Adc99878	Murine Am
Aaw05384	Human amy
Aay69716	Beta-APP
Aaw82189	Fluorogen
Aay30942	Human sec
Aag73207	Protease
Aap96371	Region of
Aaw53984	Human ALZ
Aay87944	Mammalian
Abu08708	Amlyoid b
Adb61450	Amyloid b
Abb39754	Peptide #
Aam33336	Peptide #
Aam73119	Human bon
Aam60474	Human bra
Abg54835	Human liv
Abg42965	Human pep
Aau72571	Arabidops
Aaw53981	Human ALZ
Aay99757	Rice PI m
Aag47531	Arabidops
Aam96144	Human rep
Aau22838	Human pro
Aau72561	Arabidops
Aar10024	Beta-amyl
Aar37866	Full-leng
Aab13015	Human amy
Aae14377	Amyloid p
Aae14376	Amyloid p
Aae14372	Amyloid p
Aae14373	Amyloid p
Aae14375	Amyloid p
Aae14371	Amyloid p
Aae14374	Amyloid p
Abp97921	Amino aci
Aae14382	Gamma-sec
Aae14383	Gamma-sec
Aae14384	Gamma-sec
Aae14385	Gamma-sec
Aae14379	Gamma-sec
Aae14380	Gamma-sec
Aae14381	Gamma-sec
Abp97923	Amino aci
Aag55580	Arabidops
Aag47471	Arabidops

352	5	62.5	130	2	AAU21691	Aay21691 Expressed
353	5	62.5	132	2	AAR65290	Aar65290 Rat beta
354	5	62.5	132	2	AAR65291	Aar65291 Human bet
355	5	62.5	141	3	AAG47530	Aag47530 Arabidops
356	5	62.5	146	3	AAG29954	Aag29954 Arabidops
357	5	62.5	150	5	AAU72570	Aau72570 Arabidops
358	5	62.5	172	5	AAU72560	Aau72560 Arabidops
359	5	62.5	177	3	AAG19445	Aag19445 Arabidops
360	5	62.5	179	3	AAG24400	Aag24400 Arabidops
361	5	62.5	179	6	ABU02473	Abu02473 S. pneumo
362	5	62.5	186	3	AAG19904	Aag19904 Arabidops
363	5	62.5	187	4	AAU39412	Aau39412 Propionib
364	5	62.5	187	6	ABM35931	Abm35931 Propionib
365	5	62.5	191	3	AAG19210	Aag19210 Arabidops
366	5	62.5	191	3	AAG47470	Aag47470 Arabidops
367	5	62.5	198	3	AAG24399	Aag24399 Arabidops
368	5	62.5	200	3	AAG19209	Aag19209 Arabidops
369	5	62.5	205	3	AAG19208	Aag19208 Arabidops
370	5	62.5	205	5	ABG59975	Abg59975 Human DIT
371	5	62.5	210	3	AAG50589	Aag50589 Arabidops
372	5	62.5	214	3	AAG52181	Aag52181 Arabidops
373	5	62.5	214	3	AAG24398	Aag24398 Arabidops
374	5	62.5	216	4	ABB58081	Abb58081 Drosophil
375	5	62.5	218	2	AAR34483	Aar34483 attP-inte
376	5	62.5	218	2	AAW24387	Aaw24387 Lymantria
377	5	62.5	220	5	AAU78292	Aau78292 Human Pre
378	5	62.5	221	3	AAU99749	Aay99749 Rice PI m
379	5	62.5	232	3	AAG29953	Aag29953 Arabidops
380	5	62.5	233	3	AAG50587	Aag50587 Arabidops
381	5	62.5	239	5	AAE25362	Aae25362 Flea GABA
382	5	62.5	242	3	AAG47469	Aag47469 Arabidops
383	5	62.5	247	2	AAU21690	Aay21690 Mouse CD8
384	5	62.5	251	5	AAU72559	Aau72559 Arabidops
385	5	62.5	257	3	AAG19903	Aag19903 Arabidops
386	5	62.5	261	4	AAB87428	Aab87428 Human gen
387	5	62.5	264	4	ABB61132	Abb61132 Drosophil
388	5	62.5	266	4	ABG06969	Abg06969 Novel hum
389	5	62.5	269	3	AAU94745	Aay94745 Murine CD
390	5	62.5	280	2	AAR52861	Aar52861 Ly-2+Ly-3
391	5	62.5	282	2	AAR49549	Aar49549 Sequence
392	5	62.5	287	3	AAG19902	Aag19902 Arabidops
393	5	62.5	291	3	AAG30091	Aag30091 Arabidops
394	5	62.5	292	3	AAG30090	Aag30090 Arabidops
395	5	62.5	292	5	AAU72529	Aau72529 Arabidops
396	5	62.5	292	6	ABP96848	Abp96848 Arabidops
397	5	62.5	296	5	AAU72497	Aau72497 Arabidops
398	5	62.5	300	4	AAU07094	Aau07094 Human odo
399	5	62.5	317	4	AAG93173	Aag93173 C glutami
400	5	62.5	323	4	ABB67809	Abb67809 Drosophil
401	5	62.5	328	3	AAU94744	Aay94744 Murine CD
402	5	62.5	331	3	AAU94743	Aay94743 Murine CD
403	5	62.5	338	4	ABB60298	Abb60298 Drosophil
404	5	62.5	344	2	AAR20990	Aar20990 Putative
405	5	62.5	344	2	AAR34579	Aar34579 Phage L5
406	5	62.5	377	2	AAU35582	Aay35582 Chlamydia
407	5	62.5	377	7	ADB65035	Adb65035 Human pro
408	5	62.5	378	3	AAU95847	Aay95847 Autoantig

409	5	62.5	395	4	ABB61877	Abb61877	Drosophil
410	5	62.5	396	5	ABB47400	Abb47400	Listeria
411	5	62.5	408	6	ADA34727	Ada34727	Acinetoba
412	5	62.5	409	2	AAAY35136	Aay35136	Chlamydia
413	5	62.5	427	3	AAG30089	Aag30089	Arabidops
414	5	62.5	439	3	AAAY70767	Aay70767	Scorpion
415	5	62.5	457	7	ADE57487	Ade57487	Rat Prote
416	5	62.5	460	2	AAR49667	Aar49667	Human nuc
417	5	62.5	465	4	ABG20190	Abg20190	Novel hum
418	5	62.5	467	2	AAW81634	Aaw81634	GABA-gate
419	5	62.5	473	2	AAW56451	Aaw56451	UDP-gluc
420	5	62.5	478	6	ABU39792	Abu39792	Protein e
421	5	62.5	482	5	AAE25361	Aae25361	Ctenoceph
422	5	62.5	488	2	AAW69286	Aaw69286	GABA gate
423	5	62.5	488	2	AAW69285	Aaw69285	GABA gate
424	5	62.5	488	3	AAAY70768	Aay70768	Centipede
425	5	62.5	488	4	ABB64139	Abb64139	Drosophil
426	5	62.5	489	3	AAAY70766	Aay70766	Spider pr
427	5	62.5	496	2	AAW81633	Aaw81633	GABA-gate
428	5	62.5	500	4	AAB69064	Aab69064	A. tumefa
429	5	62.5	522	4	ABB59203	Abb59203	Drosophil
430	5	62.5	544	3	AAG31954	Aag31954	Arabidops
431	5	62.5	561	2	AAW97413	Aaw97413	Lucilia c
432	5	62.5	606	4	ABB65121	Abb65121	Drosophil
433	5	62.5	631	7	ADC94275	Adc94275	E. faeciu
434	5	62.5	635	4	AAE10913	Aae10913	Human gen
435	5	62.5	651	4	ABB62422	Abb62422	Drosophil
436	5	62.5	655	5	ABJ04651	Abj04651	Protein o
437	5	62.5	670	5	ABB81499	Abb81499	Abeta42-H
438	5	62.5	673	5	ABJ04652	Abj04652	Protein o
439	5	62.5	694	3	AAG31953	Aag31953	Arabidops
440	5	62.5	708	3	AAB40853	Aab40853	Human ORF
441	5	62.5	708	5	ABP43583	Abp43583	TRABID pr
442	5	62.5	709	5	ABP41264	Abp41264	Human ova
443	5	62.5	715	6	AAE32908	Aae32908	Nostoc sp
444	5	62.5	743	3	AAG31952	Aag31952	Arabidops
445	5	62.5	800	7	ADC94468	Adc94468	E. faeciu
446	5	62.5	867	6	ABU29843	Abu29843	Protein e
447	5	62.5	882	6	ADA33945	Ada33945	Acinetoba
448	5	62.5	883	6	ABU20458	Abu20458	Protein e
449	5	62.5	909	5	ABB93609	Abb93609	Herbicida
450	5	62.5	1039	4	ABB69116	Abb69116	Drosophil
451	5	62.5	1209	4	ABB59138	Abb59138	Drosophil
452	5	62.5	1221	7	ADC94332	Adc94332	E. faeciu
453	5	62.5	1358	5	ABB80603	Abb80603	Human sbg
454	5	62.5	1381	4	AAU68547	Aau68547	Human nov
455	5	62.5	1425	4	ABB71908	Abb71908	Drosophil
456	5	62.5	1653	5	ABP64747	Abp64747	Human pro
457	5	62.5	2120	6	ABR82074	Abr82074	Human sep
458	5	62.5	2307	4	ABB65433	Abb65433	Drosophil
459	5	62.5	2748	4	ABB58843	Abb58843	Drosophil
460	5	62.5	2960	7	ADE60345	Ade60345	Human Pro
461	5	62.5	3105	5	ABB80604	Abb80604	Human sbg
462	5	62.5	3190	6	AAE36131	Aae36131	Streptomy
463	5	62.5	3192	4	AAE10128	Aae10128	Streptomy
464	4	50.0	4	2	AAR14136	Aar14136	Substrate
465	4	50.0	4	2	AAR22055	Aar22055	Chromogen

466	4	50.0	4	2	AAW82443	Aaw82443	Seq ID 12
467	4	50.0	4	3	AAB22905	Aab22905	b-secreta
468	4	50.0	4	3	AAy87945	Aay87945	Mammalian
469	4	50.0	4	3	AAy94776	Aay94776	Beta-secr
470	4	50.0	4	3	AAy79607	Aay79607	B-secreta
471	4	50.0	4	3	AAB32122	Aab32122	Beta-secr
472	4	50.0	4	5	ABB06544	Abb06544	Amyloid p
473	4	50.0	4	5	ABG94467	Abg94467	Protease
474	4	50.0	4	7	ADB33535	Adb33535	APP beta-
475	4	50.0	4	7	ADC18404	Adc18404	Protease
476	4	50.0	5	3	AAy69702	Aay69702	Beta-APP
477	4	50.0	5	4	AAU07235	Aau07235	Human bet
478	4	50.0	5	4	AAE10667	Aae10667	Human APP
479	4	50.0	5	4	AAE06907	Aae06907	Human Asp
480	4	50.0	5	4	AAU06636	Aau06636	Peptide p
481	4	50.0	5	7	ADB33544	Adb33544	Mutant AP
482	4	50.0	5	7	ADB33553	Adb33553	Mutant AP
483	4	50.0	5	7	ADB33552	Adb33552	Mutant AP
484	4	50.0	6	2	AAR42400	Aar42400	Peptide r
485	4	50.0	6	2	AAW70864	Aaw70864	Beta-amyl
486	4	50.0	6	2	AAW70868	Aaw70868	Beta-amyl
487	4	50.0	6	2	AAW82441	Aaw82441	Human amy
488	4	50.0	6	4	AAB49095	Aab49095	Human amy
489	4	50.0	6	4	AAB46199	Aab46199	Human APP
490	4	50.0	6	6	ABP57524	Abp57524	Peptide #
491	4	50.0	6	7	ADB75165	Adb75165	Human amy
492	4	50.0	6	7	ADB75161	Adb75161	Human amy
493	4	50.0	7	2	AAR42403	Aar42403	Peptide r
494	4	50.0	7	2	AAR42402	Aar42402	Peptide r
495	4	50.0	7	2	AAR74299	Aar74299	Synthetic
496	4	50.0	7	2	AAR72758	Aar72758	Antimalar
497	4	50.0	7	2	AAR72776	Aar72776	Mammalian
498	4	50.0	7	2	AAR72756	Aar72756	Antimalar
499	4	50.0	7	2	AAy49692	Aay49692	Human bet
500	4	50.0	7	3	AAy83859	Aay83859	Ribonucle
501	4	50.0	7	4	AAB46202	Aab46202	Human APP
502	4	50.0	7	5	AAO14421	Aao14421	Synthetic
503	4	50.0	7	6	AAO19884	Aao19884	Human amy
504	4	50.0	7	6	AAE35432	Aae35432	Abeta pep
505	4	50.0	7	7	ADB75173	Adb75173	Amyloid b
506	4	50.0	8	2	AAW19494	Aaw19494	Immunogen
507	4	50.0	8	2	AAW19507	Aaw19507	Immunogen
508	4	50.0	8	2	AAW70865	Aaw70865	Beta-amyl
509	4	50.0	8	3	AAy94771	Aay94771	Beta-secr
510	4	50.0	8	3	AAy94773	Aay94773	Beta-secr
511	4	50.0	8	4	AAE10661	Aae10661	Human asp
512	4	50.0	8	4	AAE02613	Aae02613	Human Asp
513	4	50.0	8	5	AAU78518	Aau78518	N terminu
514	4	50.0	8	5	ABB78622	Abb78622	Human bet
515	4	50.0	8	5	ABG32725	Abg32725	Antigenic
516	4	50.0	8	6	ABR54159	Abr54159	Beta-secr
517	4	50.0	8	7	ADB75162	Adb75162	Human amy
518	4	50.0	8	7	ADB75174	Adb75174	Amyloid b
519	4	50.0	9	2	AAR55719	Aar55719	Tyrosine-
520	4	50.0	9	2	AAW82081	Aaw82081	Fluorogen
521	4	50.0	9	2	AAW82082	Aaw82082	Fluorogen
522	4	50.0	9	3	AAB07876	Aab07876	A peptide



523	4	50.0	9	3	AAB07874	Aab07874	A peptide
524	4	50.0	9	3	AAB07878	Aab07878	A peptide
525	4	50.0	9	3	AAB07875	Aab07875	A peptide
526	4	50.0	9	3	AAB07877	Aab07877	A peptide
527	4	50.0	9	3	AAB07881	Aab07881	A peptide
528	4	50.0	9	3	AAB07894	Aab07894	Substrate
529	4	50.0	9	4	AAG73293	Aag73293	Protease
530	4	50.0	9	4	AAG73280	Aag73280	Protease
531	4	50.0	9	4	AAG73279	Aag73279	Protease
532	4	50.0	9	4	AAG73297	Aag73297	Protease
533	4	50.0	9	5	ABB06519	Abb06519	Beta-secr
534	4	50.0	9	5	ABB09003	Abb09003	Peptide #
535	4	50.0	9	5	ABU60428	Abu60428	Protease
536	4	50.0	9	5	ABU60429	Abu60429	Protease
537	4	50.0	9	5	ABU60441	Abu60441	Protease
538	4	50.0	9	5	AAE16663	Aae16663	Oligopept
539	4	50.0	9	5	AAU74837	Aau74837	Synthetic
540	4	50.0	9	5	ABB07598	Abb07598	Synthetic
541	4	50.0	9	5	AAM50897	Aam50897	Oligopept
542	4	50.0	9	5	ABG67777	Abg67777	Human ADP
543	4	50.0	9	6	ABP97975	Abp97975	Synthetic
544	4	50.0	9	6	ABP57515	Abp57515	Different
545	4	50.0	9	6	ABP57084	Abp57084	Synthetic
546	4	50.0	9	6	ABP71468	Abp71468	Beta-secr
547	4	50.0	9	6	AAO16449	Aao16449	Beta-secr
548	4	50.0	9	6	ABP71269	Abp71269	Oligopept
549	4	50.0	9	6	ABR44377	Abr44377	Oligonpep
550	4	50.0	9	6	ABP58375	Abp58375	Beta-secr
551	4	50.0	9	6	AAO26801	Aao26801	Beta-secr
552	4	50.0	9	6	ABG75940	Abg75940	Synthetic
553	4	50.0	9	6	ABP71630	Abp71630	Beta-secr
554	4	50.0	9	6	AAE36000	Aae36000	APP subst
555	4	50.0	9	6	ABP70741	Abp70741	Antigenic
556	4	50.0	9	6	ABR82372	Abr82372	Beta-secr
557	4	50.0	9	6	ABR56258	Abr56258	Amyloid P
558	4	50.0	9	6	ABR62018	Abr62018	Beta-secr
559	4	50.0	9	6	ADA23917	Ada23917	Alzheimer
560	4	50.0	9	6	ABR61887	Abr61887	Beta-secr
561	4	50.0	9	7	ABR56195	Abr56195	Amyloid p
562	4	50.0	9	7	ADC29723	Adc29723	Synthetic
563	4	50.0	9	7	ADC26557	Adc26557	Beta-secr
564	4	50.0	9	7	ADC10532	Adc10532	Synthetic
565	4	50.0	9	7	ADD80769	Add80769	Synthetic
566	4	50.0	9	7	ADE36575	Ade36575	Beta-amyl
567	4	50.0	10	2	AAR24263	Aar24263	Human amy
568	4	50.0	10	2	AAR24267	Aar24267	Human amy
569	4	50.0	10	2	AAR24260	Aar24260	Human amy
570	4	50.0	10	2	AAR58928	Aar58928	Human amy
571	4	50.0	10	2	AAW08362	Aaw08362	Beta-secr
572	4	50.0	10	2	AAV33756	Aay33756	Synthetic
573	4	50.0	10	3	AAV69706	Aay69706	Beta-APP
574	4	50.0	10	3	AAV69707	Aay69707	Beta-APP
575	4	50.0	10	3	AAV69710	Aay69710	Beta-APP
576	4	50.0	10	3	AAV69705	Aay69705	Beta-APP
577	4	50.0	10	3	AAV69709	Aay69709	Beta-APP
578	4	50.0	10	3	AAV69711	Aay69711	Beta-APP
579	4	50.0	10	3	AAV69712	Aay69712	Beta-APP

580	4	50.0	10	4	AAU07226	Aau07226	Human bet
581	4	50.0	10	4	AAE10653	Aae10653	Human APP
582	4	50.0	10	4	AAE06898	Aae06898	Human amy
583	4	50.0	10	4	AAB46213	Aab46213	Human APP
584	4	50.0	10	4	AAB61337	Aab61337	Swedish m
585	4	50.0	10	4	AAE02605	Aae02605	Human APP
586	4	50.0	10	4	AAB66575	Aab66575	Synthetic
587	4	50.0	10	4	AAB47266	Aab47266	Peptide 5
588	4	50.0	10	4	AAU06627	Aau06627	Synthetic
589	4	50.0	10	5	ABB06427	Abb06427	Beta-secr
590	4	50.0	10	5	ABB06425	Abb06425	Human APP
591	4	50.0	10	5	ABB06548	Abb06548	Beta-secr
592	4	50.0	10	5	ABG78376	Abg78376	Human bet
593	4	50.0	10	5	ABB78614	Abb78614	Beta-secr
594	4	50.0	10	5	ABG76935	Abg76935	Synthetic
595	4	50.0	10	5	AAU99491	Aau99491	Peptide #
596	4	50.0	10	5	ABG30941	Abg30941	Nogo/BACE
597	4	50.0	10	6	AAE35675	Aae35675	Human bet
598	4	50.0	10	6	ABP57509	Abp57509	Different
599	4	50.0	10	6	ABG76104	Abg76104	Amyloid p
600	4	50.0	10	6	ABR61932	Abr61932	Human amy
601	4	50.0	10	6	ABR62009	Abr62009	Substrate
602	4	50.0	10	6	ADA74820	Ada74820	Human amy
603	4	50.0	10	7	ABR84672	Abr84672	Aggrecona
604	4	50.0	10	7	AAE39496	Aae39496	Human GDF
605	4	50.0	10	7	ADD93711	Add93711	GDF-assoc
606	4	50.0	11	4	AAB91793	Aab91793	Amyloid b
607	4	50.0	11	4	AAB91820	Aab91820	Amyloid b
608	4	50.0	11	4	AAB97469	Aab97469	Asp2 subs
609	4	50.0	11	4	AAB75145	Aab75145	Asp 1 sub
610	4	50.0	11	4	AAB75142	Aab75142	APP Swedi
611	4	50.0	11	5	ABB04914	Abb04914	Human amy
612	4	50.0	12	3	AAB26009	Aab26009	Human IgE
613	4	50.0	12	4	AAU16734	Aau16734	Peptide E
614	4	50.0	12	5	ABG78396	Abg78396	Memapsin
615	4	50.0	12	5	ABB08996	Abb08996	Amyloid p
616	4	50.0	12	5	AAE16656	Aae16656	APP subst
617	4	50.0	12	5	AAU74830	Aau74830	Synthetic
618	4	50.0	12	5	ABB07591	Abb07591	Biotinyla
619	4	50.0	12	5	ABJ00264	Abj00264	Human IgE
620	4	50.0	12	6	AAE35674	Aae35674	Human bet
621	4	50.0	12	6	ABP97968	Abp97968	A synthet
622	4	50.0	12	6	AAO26794	Aao26794	Beta-secr
623	4	50.0	12	7	ADC29716	Adc29716	Synthetic
624	4	50.0	12	7	ADD80762	Add80762	Synthetic
625	4	50.0	13	2	AAR91739	Aar91739	HER4 immu
626	4	50.0	13	2	AAW18501	Aaw18501	Amino-ter
627	4	50.0	13	2	AAW97353	Aaw97353	Immunosup
628	4	50.0	13	4	AAB49094	Aab49094	Human amy
629	4	50.0	13	4	AAB46198	Aab46198	Human APP
630	4	50.0	13	4	AAG67580	Aag67580	Peptide d
631	4	50.0	13	4	AAG67572	Aag67572	Peptide d
632	4	50.0	13	5	ABB06591	Abb06591	Beta-secr
633	4	50.0	13	5	AAM50890	Aam50890	Fluoresce
634	4	50.0	13	5	ABG69390	Abg69390	Vascular
635	4	50.0	13	6	ABP57077	Abp57077	Synthetic
636	4	50.0	13	6	ABP71461	Abp71461	Beta-secr

637	4	50.0	13	6	AAO16442	Aao16442	Beta-secr
638	4	50.0	13	6	ABP71262	Abp71262	Synthetic
639	4	50.0	13	6	ABR44370	Abr44370	Synthetic
640	4	50.0	13	6	ABP58368	Abp58368	Synthetic
641	4	50.0	13	6	ABG75933	Abg75933	Synthetic
642	4	50.0	13	6	ABP71623	Abp71623	Beta-secr
643	4	50.0	13	6	AAE35993	Aae35993	APP subst
644	4	50.0	13	6	ABR42268	Abr42268	Amyloid p
645	4	50.0	13	6	ABR82365	Abr82365	Synthetic
646	4	50.0	13	6	ABR56251	Abr56251	Amyloid P
647	4	50.0	13	6	ABU63709	Abu63709	Rat amylo
648	4	50.0	13	6	ABR62011	Abr62011	Amino aci
649	4	50.0	13	6	ABR61880	Abr61880	Beta-secr
650	4	50.0	13	7	ABR56172	Abr56172	Amyloid p
651	4	50.0	13	7	ADC10524	Adc10524	Synthetic
652	4	50.0	13	7	ADC81567	Adc81567	P33K-BACE
653	4	50.0	14	2	AAW10200	Aaw10200	Serum imm
654	4	50.0	14	2	AAW97343	Aaw97343	Immunosup
655	4	50.0	14	2	AAW97321	Aaw97321	Immunosup
656	4	50.0	14	4	ABR51897	Abr51897	Mutant Pe
657	4	50.0	14	4	ABR51829	Abr51829	Mutant Pe
658	4	50.0	14	4	ABR51852	Abr51852	Mutant Pe
659	4	50.0	14	4	ABR51874	Abr51874	Mutant Pe
660	4	50.0	14	4	ABR51892	Abr51892	Mutant Pe
661	4	50.0	14	4	ABR51896	Abr51896	Mutant Pe
662	4	50.0	14	4	ABR51923	Abr51923	Mutant Pe
663	4	50.0	14	4	ABR51873	Abr51873	Mutant Pe
664	4	50.0	14	4	ABR51889	Abr51889	Mutant Pe
665	4	50.0	14	4	ABR51847	Abr51847	Mutant Pe
666	4	50.0	14	4	ABR51865	Abr51865	Mutant Pe
667	4	50.0	14	4	ABR51823	Abr51823	Mutant Pe
668	4	50.0	14	4	ABR51836	Abr51836	Mutant Pe
669	4	50.0	14	4	ABR51895	Abr51895	Mutant Pe
670	4	50.0	14	4	ABR51843	Abr51843	Mutant Pe
671	4	50.0	14	4	ABR51894	Abr51894	Mutant Pe
672	4	50.0	14	4	ABR51921	Abr51921	Mutant Pe
673	4	50.0	14	4	ABR51853	Abr51853	Mutant Pe
674	4	50.0	14	4	ABR51890	Abr51890	Mutant Pe
675	4	50.0	14	4	ABR51915	Abr51915	Mutant Pe
676	4	50.0	14	4	ABR51922	Abr51922	Mutant Pe
677	4	50.0	14	4	ABR51898	Abr51898	Mutant Pe
678	4	50.0	14	6	AAE35673	Aae35673	Human bet
679	4	50.0	14	6	ABU63708	Abu63708	Rat amylo
680	4	50.0	15	2	AAW81466	Aaw81466	Synthetic
681	4	50.0	15	2	AAW97322	Aaw97322	Immunosup
682	4	50.0	15	4	ABR51936	Abr51936	Mutant Pe
683	4	50.0	15	4	ABR51937	Abr51937	Mutant Pe
684	4	50.0	15	4	ABR51957	Abr51957	Mutant Pe
685	4	50.0	16	2	AAR28852	Aar28852	Vasorelax
686	4	50.0	16	2	AAR43486	Aar43486	Ro/SSA ep
687	4	50.0	16	2	AAR60371	Aar60371	Beta-amyl
688	4	50.0	16	2	AAW08363	Aaw08363	Beta-secr
689	4	50.0	16	2	AAW35344	Aaw35344	Human bet
690	4	50.0	16	2	AAW49693	Aay49693	Human bet
691	4	50.0	16	2	AAW97323	Aaw97323	Immunosup
692	4	50.0	16	2	AAW33757	Aay33757	Beta-amyl
693	4	50.0	16	3	AAB06316	Aab06316	Human bet

694	4	50.0	16	4	AAB91801	Aab91801	Amyloid b
695	4	50.0	16	4	AAB91828	Aab91828	Amyloid b
696	4	50.0	16	5	ABB81322	Abb81322	Amyloid p
697	4	50.0	16	5	ABU60427	Abu60427	Protease
698	4	50.0	16	6	ABP60446	Abp60446	Modified
699	4	50.0	16	6	ABP60447	Abp60447	Modified
700	4	50.0	17	2	AAR07752	Aar07752	Cerebrova
701	4	50.0	17	2	AAR42399	Aar42399	Peptide r
702	4	50.0	17	2	AAW10202	Aaw10202	Serum imm
703	4	50.0	17	2	AAW97346	Aaw97346	Immunosup
704	4	50.0	17	2	AAW97324	Aaw97324	Immunosup
705	4	50.0	17	3	AAB11496	Aab11496	Human amy
706	4	50.0	17	4	AAG76748	Aag76748	Human col
707	4	50.0	17	4	AAB48345	Aab48345	Beta-amyl
708	4	50.0	17	5	AAU93920	Aau93920	Human bet
709	4	50.0	17	7	ADE10849	Ade10849	Chimeric
710	4	50.0	18	2	AAW97325	Aaw97325	Immunosup
711	4	50.0	18	2	AAZ27010	Aay27010	N-termina
712	4	50.0	18	3	AAB05903	Aab05903	Histone d
713	4	50.0	18	4	AAB72896	Aab72896	HDAC 4 pe
714	4	50.0	18	4	AAE00609	Aae00609	Beta-amyl
715	4	50.0	18	5	ABG80708	Abg80708	Modified
716	4	50.0	18	5	ABG80715	Abg80715	Human IgG
717	4	50.0	18	5	ABG80703	Abg80703	Modified
718	4	50.0	18	6	ABU63710	Abu63710	Rat amylo
719	4	50.0	19	2	AAW97326	Aaw97326	Immunosup
720	4	50.0	19	4	AAM20452	Aam20452	Peptide #
721	4	50.0	19	4	ABB41251	Abb41251	Peptide #
722	4	50.0	19	4	AAM35035	Aam35035	Peptide #
723	4	50.0	19	4	ABB25247	Abb25247	Protein #
724	4	50.0	19	4	AAM74920	Aam74920	Human bon
725	4	50.0	19	4	AAM62116	Aam62116	Human bra
726	4	50.0	19	4	ABG56696	Abg56696	Human liv
727	4	50.0	19	4	AAE00611	Aae00611	Amyloid p
728	4	50.0	19	4	AAE00613	Aae00613	pCBC1 APP
729	4	50.0	19	4	AAE00614	Aae00614	pCBC1 APP
730	4	50.0	19	5	ABG44675	Abg44675	Human pep
731	4	50.0	19	6	ABU63711	Abu63711	Rat amylo
732	4	50.0	20	2	AAR94180	Aar94180	Human 35
733	4	50.0	20	2	AAW82211	Aaw82211	Fluorogen
734	4	50.0	20	2	AAW97327	Aaw97327	Immunosup
735	4	50.0	20	3	AAZ69714	Aay69714	Beta-APP
736	4	50.0	20	3	AAZ69715	Aay69715	Beta-APP
737	4	50.0	20	4	AAB49081	Aab49081	Amyloid b
738	4	50.0	20	4	AAB49078	Aab49078	Amyloid b
739	4	50.0	20	4	AAG73201	Aag73201	Protease
740	4	50.0	20	4	AAG73229	Aag73229	Protease
741	4	50.0	20	4	AAG73333	Aag73333	Protease
742	4	50.0	20	4	AAG73202	Aag73202	Protease
743	4	50.0	20	4	AAG73315	Aag73315	Protease
744	4	50.0	20	4	AAB46204	Aab46204	Human APP
745	4	50.0	20	4	AAB46179	Aab46179	Tetanus t
746	4	50.0	20	4	AAB46182	Aab46182	Tetanus t
747	4	50.0	20	5	AAU78509	Aau78509	Beta amyl
748	4	50.0	20	6	ABU63713	Abu63713	Rat amylo
749	4	50.0	21	2	AAR26295	Aar26295	Ala9, Thr
750	4	50.0	21	2	AAR38375	Aar38375	Endotheli

751	4	50.0	21	2	AAR69401	Aar69401	[Ala9, Th
752	4	50.0	21	2	AAW08361	Aaw08361	Beta-secr
753	4	50.0	21	2	AAW82186	Aaw82186	Fluorogen
754	4	50.0	21	2	AAW82187	Aaw82187	Fluorogen
755	4	50.0	21	2	AAW97328	Aaw97328	Immunosup
756	4	50.0	21	2	AAAY33755	Aay33755	Synthetic
757	4	50.0	21	4	AAG73204	Aag73204	Protease
758	4	50.0	21	4	AAG73205	Aag73205	Protease
759	4	50.0	21	4	AAG73316	Aag73316	Protease
760	4	50.0	21	4	AAG73203	Aag73203	Protease
761	4	50.0	21	4	AAB47265	Aab47265	Peptide 5
762	4	50.0	22	2	AAR07753	Aar07753	Bta-amylo
763	4	50.0	22	2	AAW10201	Aaw10201	Serum imm
764	4	50.0	22	2	AAW97329	Aaw97329	Immunosup
765	4	50.0	22	2	AAW97345	Aaw97345	Immunosup
766	4	50.0	22	3	AAAY56796	Aay56796	SSAD frag
767	4	50.0	22	4	AAB46196	Aab46196	Tetanus t
768	4	50.0	22	4	AAB46175	Aab46175	Tetanus t
769	4	50.0	22	4	AAB46203	Aab46203	Human APP
770	4	50.0	22	4	ABG02948	Abg02948	Novel hum
771	4	50.0	23	4	AAB97474	Aab97474	Asp2 subs
772	4	50.0	23	4	AAB75148	Aab75148	Asp 1 sub
773	4	50.0	23	7	ADC81568	Adc81568	P33K-BACE
774	4	50.0	24	2	AAR52569	Aar52569	Alzheimer
775	4	50.0	24	4	AAB49082	Aab49082	Amyloid b
776	4	50.0	24	4	AAB46183	Aab46183	Tetanus t
777	4	50.0	24	5	ABP62489	Abp62489	Human imm
778	4	50.0	25	2	AAR42404	Aar42404	C-terminu
779	4	50.0	25	2	AAW07322	Aaw07322	Peptide s
780	4	50.0	25	4	AAB49092	Aab49092	Amyloid b
781	4	50.0	26	4	AAG73200	Aag73200	Protease
782	4	50.0	26	5	ABJ04917	Abj04917	Human pro
783	4	50.0	26	7	ADE36573	Ade36573	APP epito
784	4	50.0	27	2	AAW77575	Aaw77575	Staphyloc
785	4	50.0	27	4	AAB49088	Aab49088	Amyloid b
786	4	50.0	27	4	AAB49074	Aab49074	Amyloid b
787	4	50.0	27	4	AAB49086	Aab49086	Amyloid b
788	4	50.0	27	4	AAB46189	Aab46189	Tetanus t
789	4	50.0	27	4	AAB46187	Aab46187	Tetanus t
790	4	50.0	27	5	AAM50912	Aam50912	Beta amyl
791	4	50.0	27	6	AAO19881	Aao19881	Human amy
792	4	50.0	28	1	AAP70594	Aap70594	Sequence
793	4	50.0	28	1	AAP90381	Aap90381	Synthetic
794	4	50.0	28	2	AAR60368	Aar60368	Beta-amyl
795	4	50.0	28	2	AAR54702	Aar54702	Beta-amyl
796	4	50.0	28	2	AAR64171	Aar64171	A4-P(1-28
797	4	50.0	28	2	AAR64164	Aar64164	Generic b
798	4	50.0	28	2	AAR64172	Aar64172	A4-B(1-28
799	4	50.0	28	2	AAR64170	Aar64170	A4-O(1-28
800	4	50.0	28	2	AAW01413	Aaw01413	Beta/A4-a
801	4	50.0	28	2	AAW01414	Aaw01414	Beta/A4-a
802	4	50.0	28	2	AAAY39806	Aay39806	Beta-amyl
803	4	50.0	28	2	AAAY39805	Aay39805	Beta-amyl
804	4	50.0	28	2	AAW81467	Aaw81467	Synthetic
805	4	50.0	28	4	AAB35595	Aab35595	Human clo
806	4	50.0	28	4	AAB35594	Aab35594	Human clo
807	4	50.0	28	4	AAB35593	Aab35593	Human clo

808	4	50.0	28	4	AAB35597	Aab35597	Human clo
809	4	50.0	28	4	AAB35600	Aab35600	Human clo
810	4	50.0	28	4	AAB35596	Aab35596	Human clo
811	4	50.0	28	4	AAB35598	Aab35598	Human clo
812	4	50.0	28	4	AAB35599	Aab35599	Human clo
813	4	50.0	28	4	AAB36202	Aab36202	Human clo
814	4	50.0	28	4	AAB35590	Aab35590	Human clo
815	4	50.0	28	4	AAB36201	Aab36201	Human clo
816	4	50.0	28	4	AAB46176	Aab46176	Tetanus t
817	4	50.0	28	4	AAB91816	Aab91816	Amyloid b
818	4	50.0	28	4	AAB91789	Aab91789	Amyloid b
819	4	50.0	28	4	AAB91827	Aab91827	Amyloid b
820	4	50.0	28	4	AAB91783	Aab91783	Amyloid b
821	4	50.0	28	4	AAB91800	Aab91800	Amyloid b
822	4	50.0	28	4	AAE04243	Aae04243	Human gen
823	4	50.0	28	4	AAB49396	Aab49396	Human amy
824	4	50.0	28	5	AAE21439	Aae21439	Human bet
825	4	50.0	28	5	ABB76030	Abb76030	Beta amyl
826	4	50.0	28	5	AAO18467	Aao18467	Human bet
827	4	50.0	28	5	AAO18470	Aao18470	Human bet
828	4	50.0	28	5	AAO18473	Aao18473	Human bet
829	4	50.0	28	5	AAO18476	Aao18476	Human bet
830	4	50.0	28	5	AAO18461	Aao18461	Human bet
831	4	50.0	28	5	AAO18464	Aao18464	Human bet
832	4	50.0	28	5	AAO18458	Aao18458	Human bet
833	4	50.0	28	5	AAU76484	Aau76484	Amino aci
834	4	50.0	28	5	ABB04910	Abb04910	Human amy
835	4	50.0	28	5	AAE26081	Aae26081	Beta amyl
836	4	50.0	28	5	AAM50910	Aam50910	Beta amyl
837	4	50.0	28	5	ABB77991	Abb77991	Fragment
838	4	50.0	28	6	AAE35672	Aae35672	Human bet
839	4	50.0	28	6	AAE33794	Aae33794	Beta-amyl
840	4	50.0	28	6	ABG72238	Abg72238	Mutant H6
841	4	50.0	28	6	ABG72246	Abg72246	Mutant K2
842	4	50.0	28	6	ABG72234	Abg72234	Wild-type
843	4	50.0	28	6	ABG72244	Abg72244	Mutant E2
844	4	50.0	28	6	ABG72241	Abg72241	Mutant H1
845	4	50.0	28	6	ABG72240	Abg72240	Mutant E1
846	4	50.0	28	6	ABG72237	Abg72237	Mutant R5
847	4	50.0	28	6	ABG72245	Abg72245	Mutant D2
848	4	50.0	28	6	ABG72243	Abg72243	Mutant K1
849	4	50.0	28	6	ABG72242	Abg72242	Mutant H1
850	4	50.0	28	6	ABG72239	Abg72239	Mutant D7
851	4	50.0	28	6	AAE35431	Aae35431	Abeta pep
852	4	50.0	28	6	AAE33219	Aae33219	Beta amyl
853	4	50.0	28	6	ABU63712	Abu63712	Rat amylo
854	4	50.0	28	7	AAE38831	Aae38831	Membrane
855	4	50.0	29	5	AAE26331	Aae26331	Human bet
856	4	50.0	30	2	AAW08360	Aaw08360	Beta-secr
857	4	50.0	30	2	AAW81468	Aaw81468	Synthetic
858	4	50.0	30	2	AAV33754	Aay33754	Synthetic
859	4	50.0	30	3	AAB07895	Aab07895	Substrate
860	4	50.0	30	4	AAB47264	Aab47264	Peptide 2
861	4	50.0	30	4	AAB47267	Aab47267	Peptide f
862	4	50.0	30	5	ABG94392	Abg94392	A beta pe
863	4	50.0	30	5	ABB09004	Abb09004	Peptide #
864	4	50.0	30	5	AAU11766	Aau11766	Human amy



865	4	50.0	30	5	AAU11778	Aau11778	Synthetic
866	4	50.0	30	5	AAU11777	Aau11777	Synthetic
867	4	50.0	30	5	AAE16664	Aae16664	Oligopept
868	4	50.0	30	5	AAU74838	Aau74838	Synthetic
869	4	50.0	30	5	ABB07599	Abb07599	Synthetic
870	4	50.0	30	5	AAM50898	Aam50898	Oligopept
871	4	50.0	30	5	ABG80717	Abg80717	Mouse Res
872	4	50.0	30	5	ABG80704	Abg80704	Modified
873	4	50.0	30	6	AAE35677	Aae35677	Human Abe
874	4	50.0	30	6	ABP97976	Abp97976	Synthetic
875	4	50.0	30	6	ABP57085	Abp57085	Synthetic
876	4	50.0	30	6	ABP71469	Abp71469	Beta-secr
877	4	50.0	30	6	AAO16450	Aao16450	Beta-secr
878	4	50.0	30	6	ABP71270	Abp71270	Oligopept
879	4	50.0	30	6	ABR44378	Abr44378	Oligonpep
880	4	50.0	30	6	ABP58376	Abp58376	Beta-secr
881	4	50.0	30	6	AAO26802	Aao26802	Beta-secr
882	4	50.0	30	6	ABG75941	Abg75941	Synthetic
883	4	50.0	30	6	ABP71631	Abp71631	Beta-secr
884	4	50.0	30	6	AAE36001	Aae36001	APP subst
885	4	50.0	30	6	ABR42769	Abr42769	Human amy
886	4	50.0	30	6	ABR42780	Abr42780	Amyloid b
887	4	50.0	30	6	ABR42781	Abr42781	Amyloid b
888	4	50.0	30	6	ABR82373	Abr82373	Beta-secr
889	4	50.0	30	6	ABR56259	Abr56259	Amyloid P
890	4	50.0	30	6	ABR62019	Abr62019	Beta-secr
891	4	50.0	30	6	ABR61888	Abr61888	Beta-secr
892	4	50.0	30	7	ABR56196	Abr56196	Amyloid p
893	4	50.0	30	7	ADC29724	Adc29724	Synthetic
894	4	50.0	30	7	ADC10531	Adc10531	Synthetic
895	4	50.0	30	7	ADD80770	Add80770	Synthetic
896	4	50.0	31	4	ABB40171	Abb40171	Peptide #
897	4	50.0	31	4	AAM33820	Aam33820	Peptide #
898	4	50.0	31	4	AAM73625	Aam73625	Human bon
899	4	50.0	31	4	ABG55358	Abg55358	Human liv
900	4	50.0	31	5	ABG43495	Abg43495	Human pep
901	4	50.0	32	2	AAW04402	Aaw04402	Mouse amy
902	4	50.0	32	2	AAW04403	Aaw04403	Mouse amy
903	4	50.0	32	2	AAW04401	Aaw04401	Mouse amy
904	4	50.0	32	5	ABB08999	Abb08999	Amyloid p
905	4	50.0	32	5	AAE16659	Aae16659	APP subst
906	4	50.0	32	5	AAU74833	Aau74833	Synthetic
907	4	50.0	32	5	ABB07594	Abb07594	Biotinyla
908	4	50.0	32	6	AAE35678	Aae35678	Human Abe
909	4	50.0	32	6	ABP97971	Abp97971	A synthet
910	4	50.0	32	6	AAO26797	Aao26797	Beta-secr
911	4	50.0	32	7	ADC29719	Adc29719	Synthetic
912	4	50.0	32	7	ADD80765	Add80765	Synthetic
913	4	50.0	33	2	AAW08359	Aaw08359	Beta-secr
914	4	50.0	33	2	AAW81469	Aaw81469	Synthetic
915	4	50.0	33	2	AAV33753	Aay33753	Synthetic
916	4	50.0	33	3	AAB07892	Aab07892	Substrate
917	4	50.0	33	4	AAB49075	Aab49075	Amyloid b
918	4	50.0	33	4	AAM87468	Aam87468	Human imm
919	4	50.0	33	4	AAB47263	Aab47263	Peptide 1
920	4	50.0	33	5	ABB09001	Abb09001	P26-P4'SW
921	4	50.0	33	5	AAE16661	Aae16661	P26-P4'SW

922	4	50.0	33	5	AAU74835	Aau74835	Synthetic
923	4	50.0	33	5	ABB07596	Abb07596	Biotinyla
924	4	50.0	33	5	AAM50893	Aam50893	Fluoresce
925	4	50.0	33	5	AAM50895	Aam50895	P26-P4'SW
926	4	50.0	33	5	AAU93990	Aau93990	Human bet
927	4	50.0	33	6	ABP97973	Abp97973	Synthetic
928	4	50.0	33	6	ABP57082	Abp57082	P26-P4'SW
929	4	50.0	33	6	ABP71466	Abp71466	Beta-secr
930	4	50.0	33	6	AAO16445	Aao16445	Beta-secr
931	4	50.0	33	6	AAO16447	Aao16447	Beta-secr
932	4	50.0	33	6	ABP71267	Abp71267	Synthetic
933	4	50.0	33	6	ABR44375	Abr44375	P26-P4' S
934	4	50.0	33	6	ABP58373	Abp58373	Beta-secr
935	4	50.0	33	6	AAO26799	Aao26799	Beta-secr
936	4	50.0	33	6	ABG75938	Abg75938	Beta-secr
937	4	50.0	33	6	ABP71628	Abp71628	Beta-secr
938	4	50.0	33	6	AAE35998	Aae35998	P26-P4'SW
939	4	50.0	33	6	ABR42273	Abr42273	Amyloid p
940	4	50.0	33	6	ABR42271	Abr42271	Amyloid p
941	4	50.0	33	6	ABR82370	Abr82370	Beta-secr
942	4	50.0	33	6	ABR56256	Abr56256	Amyloid P
943	4	50.0	33	6	ABR56254	Abr56254	Amyloid P
944	4	50.0	33	6	ABR62016	Abr62016	Beta-secr
945	4	50.0	33	6	ABR62014	Abr62014	Amino aci
946	4	50.0	33	6	ABR61885	Abr61885	Beta-secr
947	4	50.0	33	6	ABR61883	Abr61883	Beta-secr
948	4	50.0	33	7	ABR56177	Abr56177	Amyloid p
949	4	50.0	33	7	ABR56175	Abr56175	Amyloid p
950	4	50.0	33	7	ADC29721	Adc29721	Synthetic
951	4	50.0	33	7	ADC10529	Adc10529	Synthetic
952	4	50.0	33	7	ADD80767	Add80767	Synthetic
953	4	50.0	33	7	ADE10851	Adel0851	Chimeric
954	4	50.0	34	3	AAG50440	Aag50440	Arabidops
955	4	50.0	34	4	AAB49079	Aab49079	Amyloid b
956	4	50.0	34	4	AAB49085	Aab49085	Amyloid b
957	4	50.0	34	4	AAB49087	Aab49087	Amyloid b
958	4	50.0	34	4	AAB49080	Aab49080	Amyloid b
959	4	50.0	34	4	AAB46188	Aab46188	Tetanus t
960	4	50.0	34	4	AAB46180	Aab46180	Tetanus t
961	4	50.0	34	4	AAB46181	Aab46181	Tetanus t
962	4	50.0	34	4	AAB46186	Aab46186	Tetanus t
963	4	50.0	34	4	ABB37547	Abb37547	Peptide #
964	4	50.0	34	4	ABB22841	Abb22841	Protein #
965	4	50.0	34	5	ABG40346	Abg40346	Human pep
966	4	50.0	34	6	AAE35682	Aae35682	Human Abe
967	4	50.0	34	6	AAE35679	Aae35679	Human Abe
968	4	50.0	34	6	AAE35681	Aae35681	Human Abe
969	4	50.0	34	6	ABP78419	Abp78419	N. gonorr
970	4	50.0	34	6	ABP57080	Abp57080	Synthetic
971	4	50.0	34	6	ABP71464	Abp71464	Beta-secr
972	4	50.0	34	6	ABP71265	Abp71265	Synthetic
973	4	50.0	34	6	ABR44373	Abr44373	Synthetic
974	4	50.0	34	6	ABP58371	Abp58371	Synthetic
975	4	50.0	34	6	ABG75936	Abg75936	Synthetic
976	4	50.0	34	6	ABP71626	Abp71626	Beta-secr
977	4	50.0	34	6	AAE35996	Aae35996	APP subst
978	4	50.0	34	6	ABR82368	Abr82368	Synthetic

979	4	50.0	34	7	ADC10527	Adc10527	Synthetic
980	4	50.0	35	2	AAW02335	Aaw02335	Beta-amyl
981	4	50.0	35	2	AAW47228	Aaw47228	Beta-amyl
982	4	50.0	35	2	AAW89355	Aaw89355	Beta-amyl
983	4	50.0	35	2	AAW89360	Aaw89360	Beta-amyl
984	4	50.0	35	2	AAW89361	Aaw89361	Beta-amyl
985	4	50.0	35	2	AAW89359	Aaw89359	Beta-amyl
986	4	50.0	35	5	ABG71015	Abg71015	Long form
987	4	50.0	35	5	ABB05163	Abb05163	Beta amyl
988	4	50.0	35	6	AAE35430	Aae35430	Abeta pep
989	4	50.0	36	2	AAR66939	Aar66939	Comamonas
990	4	50.0	36	2	AAW81471	Aaw81471	Synthetic
991	4	50.0	36	5	AAU11776	Aau11776	Synthetic
992	4	50.0	36	5	AAU11771	Aau11771	Synthetic
993	4	50.0	36	6	ABR42779	Abr42779	Amyloid b
994	4	50.0	36	6	ABR42774	Abr42774	Amyloid b
995	4	50.0	37	4	AAM92068	Aam92068	Human dig
996	4	50.0	37	4	AAB65073	Aab65073	Gene #12
997	4	50.0	37	4	ABG01185	Abg01185	Novel hum
998	4	50.0	38	2	AAR60362	Aar60362	Beta-amyl
999	4	50.0	38	2	AAW92722	Aaw92722	Human tac
1000	4	50.0	38	4	AAB91826	Aab91826	Amyloid b

#### ALIGNMENTS

##### RESULT 1

AAAY94772

ID AAY94772 standard; protein; 8 AA.

XX

AC AAY94772;

XX

DT 12-FEB-2001 (first entry)

XX

DE Beta-secretase substrate peptide SEQ ID 18.

XX

KW Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease;

KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.

XX

OS Synthetic.

XX

PN WO200058479-A1.

XX

PD 05-OCT-2000.

XX

PF 23-MAR-2000; 2000WO-US007755.

XX

PR 26-MAR-1999; 99US-00277229.

XX

PA (AMGE-) AMGEN INC.

XX

PI Citron M, Vassar RJ, Bennett BD;

XX

DR WPI; 2000-594643/56.

XX

PT Isolated beta-secretase nucleic acids and encoded polypeptides, useful

PT for diagnosis and gene therapy of Alzheimer's disease.

XX

PS Example 10; Page 117; 145pp; English.

XX

CC This invention relates to 3 nucleotide sequences encoding beta-secretase  
CC proteins. Beta-secretase is an enzyme involved in the production of one  
CC of the components of amyloid plaques involved in Alzheimer's disease. The  
CC invention includes an expression vector comprising the nucleotide  
CC sequence, a host cell comprising the expression vector, and a process for  
CC producing the protein through culturing the transformed cells. Also  
CC included in the invention are a polypeptide derivative of the beta-  
CC secretase protein, a fusion protein comprising beta-secretase fused to a  
CC heterologous amino acid sequence, and a method for modulating the levels  
CC of beta-secretase polypeptide in a mammal comprising administering the  
CC polynucleotide sequence. Beta-secretase exhibits neuroprotective and  
CC nootropic activity. The beta-secretase nucleotide sequence may be used to  
CC map locations of the beta-secretase gene and related genes on chromosomes  
CC and as hybridization probes in diagnostic assays to test for the presence  
CC of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's  
CC syndrome, and amyloid angiopathy. The nucleotide sequence may also be  
CC used as anti-sense inhibitors of beta-secretase expression, in gene  
CC therapy of Alzheimer's disease, and for the identification of compounds  
CC that modulate beta-secretase activity. Antibodies to the beta-secretase  
CC protein may be used for in vitro and in vivo diagnostic purposes to  
CC detect the presence of beta-secretase polypeptide in a body fluid or cell  
CC sample. The present sequence represents a beta-secretase substrate  
CC peptide

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8

|||||||

Db 1 EVKMDAEF 8

RESULT 2

AAU07230

ID AAU07230 standard; peptide; 8 AA.

XX

AC AAU07230;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human beta-amyloid protein precursor, APP-beta secretase site peptide #3.

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP-beta.

XX

OS Homo sapiens.

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000797.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000797.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502548/55.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Claim 88; Page 94; 185pp; English.  
 XX  
 CC The invention relates to a novel purified polypeptide comprising a  
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the  
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. Also included is an isoform of amyloid protein precursor (APP)  
 CC comprising the amino acid sequence of a APP or its fragment containing an  
 CC APP cleavage site recognisable by a mammalian beta-secretase, and further  
 CC comprising two lysine residues at the carboxyl terminus of the amino acid  
 CC sequence of the mammalian APP or APP fragment. The polypeptides are used  
 CC for assaying for modulators of beta-secretase activity; identifying  
 CC agents that inhibit the APP processing activity of human Asp2 aspartyl  
 CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2  
 CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.  
 CC Agents identified by the above methods are useful for treating  
 CC Alzheimer's disease; and for identifying modulators of amyloid-beta  
 CC (Abeta) peptide production, for use in designing therapeutics for the  
 CC treatment or prevention of Alzheimer's disease. Probes and primers  
 CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp  
 CC nucleic acids in in vitro assays and in Northern and Southern blots. The  
 CC present sequence represents the amino acid sequence of human amyloid  
 CC protein precursor, APP-beta secretase site peptide substrate #3 used in  
 CC assays of human Asp2 beta- secretase activity  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 1 EVKMDAEF 8

RESULT 3

AAE10660

ID AAE10660 standard; peptide; 8 AA.

XX

AC AAE10660;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human Aspartyl protease-1 (hu-Asp-1) beta-secretase, wild-type peptide.

XX

KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 4. .5

XX

PN GB2357767-A.

XX

PD 04-JUL-2001.

XX

PF 22-SEP-2000; 2000GB-00023315.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2001-444208/48.

XX

PT Polypeptide comprising fragments of human aspartyl protease with amyloid  
PT precursor protein processing activity and alpha-secretase activity, for  
PT identifying modulators useful in treating Alzheimer's disease.

XX

PS Example 15; Page 92; 187pp; English.

XX

CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl  
CC proteins which lack transmembrane domain or amino terminal domain or  
CC cytoplasmic domain and retains alpha-secretase activity and amyloid  
CC protein precursor (APP) processing activity. The proteins of the  
CC invention are useful for assaying hu-Aspl alpha-secretase activity, which  
CC in turn is useful for identifying modulators of hu-Aspl alpha-secretase  
CC activity, where modulators that increase hu-Aspl alpha-secretase activity  
CC are useful for treating Alzheimer's disease (AD) which causes progressive  
CC dementia with consequent formation of amyloid plaques, neurofibrillary  
CC tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful  
CC for assaying hu-Aspl proteolytic activity, by contacting hu-Aspl protein  
CC with the substrate under acidic conditions and determining the level of  
CC hu-Aspl proteolytic activity. The present sequence is human aspartyl  
CC protease-1 (hu-Asp-1) beta-secretase, wild-type peptide which is used for



CC determining the enzymatic activity of Asp-1 protein lacking a  
CC transmembrane (TM) domain and containing (His)6 tag  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 1 EVKMDAEF 8

RESULT 4

AAE06902

ID AAE06902 standard; peptide; 8 AA.

XX

AC AAE06902;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein (APP) substrate peptide.

XX

KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;

KW neuroprotective; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000799.

XX

PR 09-MAY-2001; 2001WO-IB000799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-483072/52.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.

XX

PS Claim 128; Page 101; 185pp; English.

XX

CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid

CC precursor protein (APP) isoforms and their corresponding DNA molecules.  
 CC Human aspartyl proteases can act as beta-secretase proteases useful for  
 CC treating Alzheimer's disease. APP isoforms are useful for identifying  
 CC modulators of amyloid-beta peptide production, for use in designing  
 CC therapeutics for the treatment and prevention of Alzheimer's disease,  
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis  
 CC and neuronal loss. APP isoforms are also used in methods for identifying  
 CC inhibitors and modulators of human Asp2 activity. The invention relates  
 CC to a method for identifying agents that modulate the activity of human  
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used  
 CC as a means to screen in cellular assays for the inhibitors of beta- and  
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in  
 CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-  
 CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.  
 CC The present sequence is human amyloid precursor protein (APP) substrate  
 CC peptide related to the invention  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 1 EVKMDAEF 8

# RESULT 5

AAE02612

ID AAE02612 standard; peptide; 8 AA.

XX

AC AAE02612;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human Aspartyl protease-1 (hu-Asp-1) beta-secretase, wild-type peptide.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;

KW beta-secretase.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 4. .5

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
XX  
PI Gurney M, Bienkowski MJ;  
XX  
DR WPI; 2001-290516/30.  
XX  
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor  
PT protein, useful for the treatment of Alzheimer's disease.  
XX  
PS Example 15; Page 94; 189pp; English.  
XX  
CC The present invention relates to enzymes for cleaving the alpha-  
CC secretase site of the amyloid precursor protein (APP) and methods of  
CC identifying those enzymes. The methods may be used to identify enzymes  
CC that may be used to cleave the alpha-secretase cleavage site of the APP  
CC protein. The enzymes may be used to treat or modulate the progress of  
CC Alzheimer's disease. The present sequence is human Aspartyl protease-1  
CC (hu-Asp-1) beta-secretase, wild-type peptide which is used for  
CC determining the enzymatic activity of Asp-1 deltaTM (His)6 protein  
XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 1 EVKMDAEF 8

# RESULT 6

AAU06635

ID AAU06635 standard; peptide; 8 AA.

XX

AC AAU06635;

XX

DT 24-OCT-2001 (first entry)

XX

DE Synthetic fluorescent Asp2 substrate.

XX

KW Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective;  
KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Glu is covalently linked to a fluorescent MCA  
FT moiety"

FT Modified-site 8

FT /note= "Glu is covalently linked to a fluorescent K-DNP  
FT moiety"

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502549/55.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Example 12; Page 81; 185pp; English.  
 XX  
 CC The invention relates to a purified polypeptide comprising a fragment of  
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2  
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and  
 CC the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. The invention also details polynucleotides for the Asp proteins  
 CC and vectors expressing them, and a polypeptide (isoform of amyloid  
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or  
 CC its fragment containing an APP cleavage site recognizable by a mammalian  
 CC beta-secretase, and further comprising two lysine residues at the  
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP  
 CC fragment. Also included in the invention are methods of identifying  
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
 CC useful for treating Alzheimer's disease. APP is useful in methods for  
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-  
 CC beta (Abeta) peptide production. APP is also useful in designing  
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP  
 CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is  
 CC associated with increased levels of Abeta processing is useful in assays  
 CC relating the Alzheimer's research. The expression vector is useful for  
 CC recombinantly expressing APP. Nucleic acids that hybridise to Asp  
 CC oligonucleotides are useful as probes or primers. The probes are useful  
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and  
 CC Southern blots. The present sequence is a synthetic fluorescent substrate  
 CC used to assay Asp2  
 XX  
 SQ Sequence 8 AA;  
  
 Query Match 100.0%; Score 8; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 EVKMDAEF 8  
 |||||  
 Db 1 EVKMDAEF 8

RESULT 7

AAU06631

ID AAU06631 standard; peptide; 8 AA.

XX

AC AAU06631;

XX

DT 24-OCT-2001 (first entry)

XX

DE Beta secretase substrate peptide.

XX

KW Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective;

KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta;

KW Beta secretase substrate peptide.

XX

OS Synthetic.

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502549/55.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.

XX

PS Claim 88; Page 94; 185pp; English.

XX

CC The invention relates to a purified polypeptide comprising a fragment of  
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2  
CC transmembrane domain and the Asp2 protein, and where the polypeptide and  
CC the fragment retain the beta-secretase activity of the mammalian Asp2  
CC protein. The invention also details polynucleotides for the Asp proteins  
CC and vectors expressing them, and a polypeptide (isoform of amyloid  
CC protein precursor (APP)) comprising the amino acid sequence of an APP or  
CC its fragment containing an APP cleavage site recognizable by a mammalian  
CC beta-secretase, and further comprising two lysine residues at the  
CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP  
CC fragment. Also included in the invention are methods of identifying  
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
CC useful for treating Alzheimer's disease. APP is useful in methods for  
CC identifying inhibitors or modulators of human Asp2 activity and amyloid-

CC beta (Abeta) peptide production. APP is also useful in designing  
CC therapeutics for the treatment or prevention of Alzheimer's disease. APP  
CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is  
CC associated with increased levels of Abeta processing is useful in assays  
CC relating the Alzheimer's research. The expression vector is useful for  
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp  
CC oligonucleotides are useful as probes or primers. The probes are useful  
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and  
CC Southern blots. The present sequence is a Beta secretase substrate  
CC peptide

XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 1 EVKMDAEF 8

RESULT 8

ABB78621

ID ABB78621 standard; peptide; 8 AA.

XX

AC ABB78621;

XX

DT 16-JUL-2002 (first entry)

XX

DE APP Swedish mutant form beta-secretase processing site SEQ ID NO:70.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.

XX

OS Synthetic.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX

PF 29-OCT-2001; 2001GB-00025934.

XX

PR 23-SEP-1999; 99US-00404133.

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

PR 22-SEP-2000; 2000GB-00023315.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Bienkowski MJ, Gurney M;

XX

DR WPI; 2002-397167/43.

XX

PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl  
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.



XX  
PS Example 12; Page 85; 182pp; English.

XX  
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)  
CC substrate (I) which comprises a peptide of no more than 50 amino acids,  
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-  
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1  
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with  
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1  
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a  
CC nucleotide sequence that hybridises under stringent conditions to the non  
CC -coding strand complementary to a defined 1804 nucleotide sequence (see  
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1  
CC proteolytic activity and lacks nucleotides encoding a transmembrane  
CC domain); (3) a purified polynucleotide (III') comprising a sequence that  
CC hybridises under stringent conditions to (III) (the nucleotide sequence  
CC encodes a polypeptide further lacking a pro-peptide domain corresponding  
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)  
CC comprising (III) or (III'); and (5) a host cell (V) transformed or  
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease  
CC substrate (I) may be used as an enzyme substrate in assays to detect  
CC aspartyl protease activity, (II) and therefore diagnose diseases  
CC associated with aberrant hu-Asp1 expression and activity such as  
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while  
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present  
CC sequence represents the amino acid sequence of a peptide that includes  
CC the beta-secretase processing site within the Swedish mutant form of  
CC amyloid precursor protein (APP), which is used in an example from the  
CC present invention

XX  
SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 1 EVKMDAEF 8

RESULT 9

AAW82083

ID AAW82083 standard; peptide; 9 AA.

XX

AC AAW82083;

XX

DT 18-FEB-1999 (first entry)

XX

DE Fluorogenic protease indicator protease binding peptide #61.

XX

KW Protease activity; fluorophore; detection; fluorogenic; cellular uptake;  
KW conformation change.

XX

OS Synthetic.

XX

PN W09837226-A1.

XX  
PD 27-AUG-1998.  
XX  
PF 20-FEB-1998; 98WO-US003000.  
XX  
PR 20-FEB-1997; 97US-00802981.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Komoriya A, Packard BS;  
XX  
DR WPI; 1998-467579/40.  
XX  
PT New fluorogenic compositions - containing 2 fluorophores separated by a  
PT peptide comprising a protease binding site, used for detecting protease  
PT activity in samples.  
XX  
PS Claim 4; Page 77; 90pp; English.  
XX  
CC AAW82023-W82240 are peptides used in the construction of a fluorogenic  
CC composition which is used for the detection of protease activity in  
CC biological samples. The products can be used for the detection of  
CC conformation changes in nucleic acids, oligosaccharides, polysaccharides,  
CC proteins, peptides, lipids, phospholipids, glycolipids, glycoproteins,  
CC steroids or polymers. In addition, attachment of a hydrophobic group to a  
CC molecule can be used to enhance uptake by cells. The composition is  
CC composed of P = peptide comprising a protease binding site for the  
CC protease, F1, F2 peptides = fluorophores where F1 is attached to the  
CC amino terminal amino acid and F2 is attached to the carboxyl terminal  
CC amino acid and S1, S2 peptides = when present, are peptide spacers where  
CC S1, when present, is attached to the amino terminal acid, and S2, when  
CC present, is attached to the carboxyl terminal amino acid  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

# RESULT 10

AAAY87949

ID AAY87949 standard; protein; 9 AA.

XX

AC AAY87949;

XX

DT 11-SEP-2000 (first entry)

XX

DE Mammalian amyloid precursor protein substrate peptide.

XX

KW Amyloid precursor protein; APP; secretase; vesicle; Abeta peptide;

KW Alzheimer's disease.

XX

OS Mammalia.  
 XX  
 PN WO200023576-A2.  
 XX  
 PD 27-APR-2000.  
 XX  
 PF 15-OCT-1999; 99WO-US024403.  
 XX  
 PR 16-OCT-1998; 98US-00173887.  
 PR 20-APR-1999; 99US-00294987.  
 XX  
 PA (HOOK/) HOOK V Y H.  
 XX  
 PI Hook VYH;  
 XX  
 DR WPI; 2000-339679/29.  
 XX  
 PT Determining the proteolytic activity of secretase for treating  
 PT Alzheimer's disease comprises permeablizing vesicles and incubating with  
 PT amyloid precursor protein (APP) to determine cleavage of APP substrate.  
 XX  
 PS Example XV; Page 97; 97pp; English.  
 XX  
 CC This invention describes a novel method for the determination of the  
 CC proteolytic activity of a secretase comprising obtaining and  
 CC permeablizing pure vesicles, incubating the vesicles with an amyloid  
 CC precursor protein (APP) and determining the cleavage of the APP substrate  
 CC where the amount of cleavage is proportional to the proteolytic activity  
 CC of the secretase. The methods are useful for selecting secretases and  
 CC agents that cleave the amyloid precursor protein substrate, inhibiting  
 CC production of the Abeta peptide found in Alzheimer's disease and treating  
 CC Alzheimer's disease in patients. This sequence represents a mammalian  
 CC amyloid precursor protein, APP substrate which is used in the method of  
 CC the invention  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 11

AAB07873

ID AAB07873 standard; peptide; 9 AA.

XX

AC AAB07873;

XX

DT 14-NOV-2000 (first entry)

XX

DE A peptide fragment derived from beta-amyloid precursor protein.

XX

KW Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;

KW amyloid plaque component; Alzheimer's disease; amyloidogenic disease;  
 KW inhibitor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200047618-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 10-FEB-2000; 2000WO-US003819.  
 XX  
 PR 10-FEB-1999; 99US-0119571P.  
 PR 15-JUN-1999; 99US-0139172P.  
 XX  
 PA (ELAN-) ELAN PHARM INC.  
 XX  
 PI Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M;  
 PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;  
 XX  
 DR WPI; 2000-533011/48.  
 XX  
 PT Purified beta-secretase protein used in assays to discover inhibitors  
 PT which can be used for the treatment of amyloidogenic diseases e.g.  
 PT Alzheimer's disease.  
 XX  
 PS Disclosure; Page 12; 121pp; English.  
 XX  
 CC The specification describes a beta-secretase enzyme. The enzyme cleaves  
 CC beta-amyloid precursor protein to produce beta-amyloid peptide. This  
 CC enzyme is therefore implicated in the production of amyloid plaque  
 CC components which accumulate in the brains of individuals afflicted with  
 CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a  
 CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-  
 CC like pathology to test if they maintain or improve cognitive ability or  
 CC reduce the plaque burden. The compounds are used for the treatment of  
 CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence  
 CC represents a peptide derived from beta-amyloid precursor protein  
 XX  
 SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

RESULT 12  
 ABU60430  
 ID ABU60430 standard; peptide; 9 AA.  
 XX  
 AC ABU60430;  
 XX  
 DT 29-APR-2003 (first entry)  
 XX

DE Protease binding peptide motif SEQ ID 142.  
XX  
KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;  
KW nuclease; screening; fluorophore; substrate cleavage.  
XX  
OS Synthetic.  
XX  
PN WO200261038-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 21-DEC-2001; 2001WO-US049781.  
XX  
PR 22-DEC-2000; 2000US-00747287.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Packard BS, Komoriya A;  
XX  
DR WPI; 2002-698548/75.  
XX  
PT Indicator composition comprising polypeptide or nucleic acid backbone  
PT joining two same chromophores resulting in quenching of fluorescence  
PT of/change in absorbance of chromophores, useful for detecting protease  
PT activity.  
XX  
PS Disclosure; Page 34; 97pp; English.  
XX  
CC This invention describes a novel indicator composition (referred as homo-  
CC doubly labeled compositions) comprising a polypeptide backbone or a  
CC nucleic acid backbone joining two chromophores of the same species  
CC whereby the chromophores form an H-dimer resulting in quenching of the  
CC fluorescence of or a change in the absorbance of the chromophore, a  
CC decrease in fluorescence or a change in absorbance indicates that the  
CC first molecule and the second molecule are interacting. The indicator is  
CC useful for detecting the activity of a protease, where an increase in  
CC fluorescence or a change in absorbance indicates that the protease  
CC cleaves the polypeptide backbone. The indicator is attached to a solid  
CC support inside a mammalian, yeast or insect cell. The composition bears a  
CC hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-  
CC fluorene-carboxylic group, 9-fluorene-carboxylic group, and 9-fluorenone-1-  
CC carboxylic group, benzyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-  
CC methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-  
CC benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-  
CC dimethoxybenzhydryl (Mbh), etc. The method described in the invention is  
CC useful for detecting protease or nuclease activity (or the presence of  
CC nucleic acid) in histological section, cells in culture, (e.g., seeded or  
CC cultured adherent cells), a biological sample such as tissue, biopsy,  
CC lymph, embryo, or whole animal, or cell suspension derived from a  
CC biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.  
CC The indicator composition is also useful for screening a test agent for  
CC the ability to modulate a protease (or a nuclease, lipase, etc.). The  
CC indicator reagents allow rapid determination of protease activity in a  
CC matter of minutes in a single-step procedure. The fluorescent indicators  
CC both absorb and emit in the visible range (400-800 nm). These signals are  
CC therefore not readily quenched by, nor is activation of the fluorophores,  
CC that is, absorption of light, interfered with by background molecules;

CC therefore they are easily detected in biological samples. The fluorogenic  
CC protease indicators utilise high efficiency fluorophores and are able to  
CC achieve a high degree of quenching while providing a strong signal when  
CC the quench is released by cleavage of the peptide substrate. The high  
CC signal allows detection of very low levels of protease activity. Thus the  
CC fluorogenic protease indicators are particularly well suited for in situ  
CC detection of protease activity. ABU60357-ABU60477 represent peptides use  
CC to illustrate the method described in the disclosure of the invention  
XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | |  
Db 2 EVKMDAEF 9

RESULT 13

ADC26556

ID ADC26556 standard; peptide; 9 AA.

XX

AC ADC26556;

XX

DT 18-DEC-2003 (first entry)

XX

DE Beta-secretase cleavage site peptide SEQ ID 3.

XX

KW nootropic; neuroprotective; Alzheimer's disease;  
KW beta-secretase cleavage site.

XX

OS Unidentified.

XX

PN WO2003065012-A2.

XX

PD 07-AUG-2003.

XX

PF 03-FEB-2003; 2003WO-US003236.

XX

PR 01-FEB-2002; 2002US-00066319.

XX

PA (UNMI ) UNIV MICHIGAN.

XX

PI Ross BD, Rehemtulla A;

XX

DR WPI; 2003-663499/62.

XX

PT New chimeric polypeptides and nucleic acids, useful for detecting and  
PT measuring protease activity, for identifying modulators of protease  
PT activity for detecting and for preventing or ameliorating Alzheimer's  
PT disease.

XX

PS Claim 14; SEQ ID NO 3; 41pp; English.

XX

CC The invention relates to a novel chimeric nucleic acid encoding a



CC polypeptide which comprises first, second and third domains, where the  
 CC first domain comprises a Golgi retention signal peptide or an endoplasmic  
 CC reticulum (ER) retention signal peptide, the second domain comprises a  
 CC protease cleavage site and the third domain comprises a reporter molecule  
 CC and where the protease cleavage site is between the Golgi retention  
 CC signal peptide and the reporter molecule. The molecules of the invention  
 CC demonstrate nootropic and neuroprotective activities and may be useful  
 CC for detecting and measuring protease activity or for identifying  
 CC modulators of protease activity in order to detect, prevent or ameliorate  
 CC Alzheimer's disease. The current sequence is that of the beta-secretase  
 CC cleavage site peptide SEQ ID 3 of the invention.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 8; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

#### RESULT 14

AAR22054

ID AAR22054 standard; peptide; 10 AA.

XX

AC AAR22054;

XX

DT 25-MAR-2003 (revised)

DT 06-JUL-1992 (first entry)

XX

DE Peptide P1.

XX

KW Beta amyloid; protein precursor; protease; Alzheimers disease;  
 KW radioiodination.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "site of radioiodination"

XX

PN W09203542-A.

XX

PD 05-MAR-1992.

XX

PF 19-AUG-1991; 91WO-U0005932.

XX

PR 17-AUG-1990; 90US-00568806.

XX

PA (UYBO-) UNIV BOSTON.

XX

PI Abraham CR;

XX

DR WPI; 1992-096886/12.

XX

PT Treatment and diagnosis of Alzheimer's disease - by reducing beta-protein  
PT precursor proteolysis near beta-protein N-terminus by administering  
PT proteolysis inhibitor.

XX

PS Disclosure; Page 6; 29pp; English.

XX

CC The synthetic peptide substrate P1 was used to assay for proteases that  
CC cleave in the vicinity of the N-terminus of the amyloid beta protein. The  
CC peptide corresponds to the beta protein precursor sequence flanking that  
CC site. The peptide starts five amino acids upstream from the N-terminus  
CC (at Asp) of the beta protein, and extends across the putative cleavage  
CC site into the beta protein itself. Histidine was substituted for the  
CC native isoleucine to give a site for radioiodination. Labelled peptide  
CC was incubated with brain fractions from Alzheimers disease patients. The  
CC resulting fragments were separated by TLC and N-terminal fragments  
CC detected by autoradiography. See also AAR22055,6. (Updated on 25-MAR-2003  
CC to correct PA field.)

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 3 EVKMDAEF 10

#### RESULT 15

AAR24261

ID AAR24261 standard; protein; 10 AA.

XX

AC AAR24261;

XX

DT 25-MAR-2003 (revised)

DT 09-NOV-1992 (first entry)

XX

DE Human amyloidin protease substrate sequence #1.

XX

KW Alzheimer's disease; beta amyloid precursor protein; APP; zinc;

KW metalloprotease; hAP; protease inhibitor; APP592-601.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Acetylated-Ser"

XX

PN W09207068-A1.

XX

PD 30-APR-1992.

XX

PF 04-OCT-1991; 91WO-US007290.

XX

PR 05-OCT-1990; 90US-00594122.

PR 30-SEP-1991; 91US-00766351.

XX  
PA (ATHE-) ATHENA NEUROSCIENCES INC.  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Dovey HF, Seubert PA, Sinha S, Mcconlogue L, Little SP;  
PI Johnstone EM;  
XX  
DR WPI; 1992-167148/20.  
XX  
PT Human amyloidin protease - used for cleaving Met-Asp bond in amyloid-like  
PT substrate for identifying protease inhibitors.  
XX  
PS Claim 1; Page 52; 62pp; English.  
XX  
CC Claimed human amyloidin protease is defined by its ability to cleave the  
CC Met-Asp bond of this synthetic substrate. The substrate, which  
CC corresponds to residues 592 to 601 of the 695 amino acid APP, can be used  
CC in an assay for identifying inhibitors of proteases which cleave Met-Asp  
CC bonds, e.g. amyloidin, human skin chymase or rat mast cell protease I or  
CC II. See AAR24260-3, AAR24266-7 and AAQ24875-Q24887. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

# RESULT 16

AAW82440

ID AAW82440 standard; peptide; 10 AA.

XX

AC AAW82440;

XX

DT 24-FEB-1999 (first entry)

XX

DE Human amyloid beta-protein N-terminal domain peptide P1.

XX

KW Amyloid beta-protein precursor; endoprotease; human; brain; screening;

KW Alzheimer's disease; O-phenanthroline; metal chelator; treatment;

KW pheymethylsulphonyl fluoride; protease inhibitor.

XX

OS Homo sapiens.

XX

PN US5849560-A.

XX

PD 15-DEC-1998.

XX

PF 26-FEB-1993; 93US-00025321.

XX

PR 17-AUG-1990; 90US-00568806.

PR 05-APR-1991; 91US-00681093.

XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Abraham CR;  
 XX  
 DR WPI; 1999-069739/06.  
 XX  
 PT Purified endoprotease associated with Alzheimer's disease - is prepared  
 PT from fractions of brain tissue homogenate and is useful for drug  
 PT screening.  
 XX  
 PS Claim 1; Col 17-18; 27pp; English.  
 XX  
 CC This sequence is the N-terminal domain of the amyloid beta-protein  
 CC precursor which is cleaved by a purified endoprotease from human brain  
 CC tissue homogenate and is identical to an endoprotease found in the brains  
 CC of humans with Alzheimer's disease. The endoprotease is inhibited by O-  
 CC phenanthroline and by metal chelators and is not inhibited by  
 CC pheymethylsulphonyl fluoride. The endoprotease is useful to screen for  
 CC protease inhibitors that might be useful for treating Alzheimer's disease  
 CC by inhibiting cleavage of the N-terminal domain of amyloid beta -protein  
 CC precursor  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 3 EVKMDAEF 10

# RESULT 17

AAY69703

ID AAY69703 standard; peptide; 10 AA.

XX

AC AAY69703;

XX

DT 11-APR-2000 (first entry)

XX

DE Beta-APP alpha-secretase substrate [KMD]-APP(-5,+5).

XX

KW Nootropic; neuroprotective; beta-amyloid precursor protein; metabolism;  
 KW cleavage site; beta-secretase; neurodegenerative disease;  
 KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO9964587-A1.

XX

PD 16-DEC-1999.

XX

PF 04-JUN-1999; 99WO-FR001326.

XX

PR 05-JUN-1998; 98FR-00007068.

PR 03-MAR-1999; 99US-0122599P.  
 XX  
 PA (RHON ) RHONE-POULENC RORER SA.  
 PA (UYPA-) UNIV CURIE PARIS VI P & M.  
 XX  
 PI Rholam M, Munoz-Gimenez N, Moutaouakil M, Cohen P, Bertrand P;  
 XX  
 DR WPI; 2000-097537/08.  
 XX  
 PT Polypeptide with beta-secretase activity, specific for wild-type amyloid  
 PT precursor protein, useful in treating Alzheimer's disease.  
 XX  
 PS Example 3; Page 24; 44pp; French.  
 XX  
 CC Peptides AAY69702-Y69718 represent synthetic peptide substrates for a  
 CC novel polypeptide with beta-secretase activity that can cleave  
 CC specifically the natural beta-amyloid precursor protein (bAPP). Normal  
 CC cleavage of the protein occurs between amino acids Met596-Asp597 and  
 CC Val636-Ile637 (positions 4-5 and 44-45 of AAY69701). The novel  
 CC polypeptide is used to identify agents that interact specifically with  
 CC it. These agents regulate metabolism of APP, particularly they slow down  
 CC or reduce production of beta-amyloid, so can be used to treat  
 CC neurodegenerative diseases, particularly Alzheimer's disease  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 18

AAU07227

ID AAU07227 standard; peptide; 10 AA.

XX

AC AAU07227;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human beta-amyloid protein precursor, APP-beta40 and 42 secretase site.

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP-beta40; APP-beta42.

XX

OS Homo sapiens.

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000797.

XX

PR 09-MAY-2001; 2001WO-IB000797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502548/55.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.

XX

PS Claim 127; Page 101; 185pp; English.

XX

CC The invention relates to a novel purified polypeptide comprising a  
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the  
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide  
CC and the fragment retain the beta-secretase activity of the mammalian Asp2  
CC protein. Also included is an isoform of amyloid protein precursor (APP)  
CC comprising the amino acid sequence of a APP or its fragment containing an  
CC APP cleavage site recognisable by a mammalian beta-secretase, and further  
CC comprising two lysine residues at the carboxyl terminus of the amino acid  
CC sequence of the mammalian APP or APP fragment. The polypeptides are used  
CC for assaying for modulators of beta-secretase activity; identifying  
CC agents that inhibit the APP processing activity of human Asp2 aspartyl  
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2  
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.  
CC Agents identified by the above methods are useful for treating  
CC Alzheimer's disease; and for identifying modulators of amyloid-beta  
CC (Abeta) peptide production, for use in designing therapeutics for the  
CC treatment or prevention of Alzheimer's disease. Probes and primers  
CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp  
CC nucleic acids in in vitro assays and in Northern and Southern blots. The  
CC present sequence represents the amino acid sequence of human amyloid  
CC protein precursor, APP-beta40 and APP-beta42 secretase sites

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 2 EVKMDAEF 9

RESULT 19

AAE10654

ID AAE10654 standard; peptide; 10 AA.

XX

AC AAE10654;



XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Human wild-type APP beta-secretase peptide, PHA-95812E.  
 XX  
 KW Human; aspartyl protease 1; Aspl; amyloid precursor protein;  
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;  
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;  
 KW APP beta-secretase peptide.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 5. .6  
 XX  
 PN GB2357767-A.  
 XX  
 PD 04-JUL-2001.  
 XX  
 PF 22-SEP-2000; 2000GB-00023315.  
 XX  
 PR 23-SEP-1999; 99US-00404133.  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Bienkowski MJ, Gurney M;  
 XX  
 DR WPI; 2001-444208/48.  
 XX  
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid  
 PT precursor protein processing activity and alpha-secretase activity, for  
 PT identifying modulators useful in treating Alzheimer's disease.  
 XX  
 PS Example 12; Page 84; 187pp; English.  
 XX  
 CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl  
 CC proteins which lack transmembrane domain or amino terminal domain or  
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid  
 CC protein precursor (APP) processing activity. The proteins of the  
 CC invention are useful for assaying hu-Aspl alpha-secretase activity, which  
 CC in turn is useful for identifying modulators of hu-Aspl alpha-secretase  
 CC activity, where modulators that increase hu-Aspl alpha-secretase activity  
 CC are useful for treating Alzheimer's disease (AD) which causes progressive  
 CC dementia with consequent formation of amyloid plaques, neurofibrillary  
 CC tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful  
 CC for assaying hu-Aspl proteolytic activity, by contacting hu-Aspl protein  
 CC with the substrate under acidic conditions and determining the level of  
 CC hu-Aspl proteolytic activity. The present sequence is wild-type human  
 CC amyloid precursor protein (APP) beta-secretase specific substrate  
 CC peptide, PHA-95812E. This peptide is used for assaying the beta-secretase  
 CC activity of human Aspartyl protease 2a (Asp2a) protein. The peptide is  
 CC also used for determining the relationship between Aspartyl protease 1  
 CC (Aspl) and APP protein

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 20

AAE06899

ID AAE06899 standard; peptide; 10 AA.

XX

AC AAE06899;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human amyloid precursor protein wild-type beta-secretase peptide.

XX

KW Human; aspartyl protease 2; Asp 2; beta-amyloid precursor protein; APP;  
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;  
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;  
KW neuroprotective; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000799.

XX

PR 09-MAY-2001; 2001WO-IB000799.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-483072/52.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
PT activity.

XX

PS Claim 127; Page 80; 185pp; English.

XX

CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid  
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.  
 CC Human aspartyl proteases can act as beta-secretase proteases useful for  
 CC treating Alzheimer's disease. APP isoforms are useful for identifying  
 CC modulators of amyloid-beta peptide production, for use in designing  
 CC therapeutics for the treatment and prevention of Alzheimer's disease,  
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis  
 CC and neuronal loss. APP isoforms are also used in methods for identifying  
 CC inhibitors and modulators of human Asp2 activity. The invention relates  
 CC to a method for identifying agents that modulate the activity of human  
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used  
 CC as a means to screen in cellular assays for the inhibitors of beta- and  
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in  
 CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-  
 CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.  
 CC The present sequence is human amyloid precursor protein (APP) wild type  
 CC beta-secretase peptide used in beta-secretase assay  
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 21

AAB46208

ID AAB46208 standard; peptide; 10 AA.

XX

AC AAB46208;

XX

DT 04-APR-2001 (first entry)

XX

DE Human APP derived immunogenic peptide #4.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200072880-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014810.

XX

PR 28-MAY-1999; 99US-00322289.

XX

PA (NEUR-) NEURALAB LTD.

XX

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX

DR WPI; 2001-032104/04.  
 XX  
 PT Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.  
 XX  
 PS Disclosure; Fig 19; 143pp; English.  
 XX  
 CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have nootropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 22

AAB46207

ID AAB46207 standard; peptide; 10 AA.

XX

AC AAB46207;

XX

DT 04-APR-2001 (first entry)

XX

DE Human APP derived immunogenic peptide #3.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200072880-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014810.

XX

PR 28-MAY-1999; 99US-00322289.

XX

PA (NEUR-) NEURALAB LTD.  
 XX  
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX  
 DR WPI; 2001-032104/04.  
 XX  
 PT Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.  
 XX  
 PS Disclosure; Fig 19; 143pp; English.  
 XX  
 CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have nootropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
 |||||  
 Db 3 EVKMDAEF 10

# RESULT 23

AAB46209

ID AAB46209 standard; peptide; 10 AA.

XX

AC AAB46209;

XX

DT 04-APR-2001 (first entry)

XX

DE Human APP derived immunogenic peptide #5.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200072880-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014810.  
 XX  
 PR 28-MAY-1999; 99US-00322289.  
 XX  
 PA (NEUR-) NEURALAB LTD.  
 XX  
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX  
 DR WPI; 2001-032104/04.  
 XX  
 PT Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.  
 XX  
 PS Disclosure; Fig 19; 143pp; English.  
 XX  
 CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have nootropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 1 EVKMDAEF 8

# RESULT 24

AAB61336

ID AAB61336 standard; peptide; 10 AA.

XX

AC AAB61336;

XX

DT 02-APR-2001 (first entry)

XX

DE Sythetic peptide from beta amyloid precursor protein.

XX

KW Memapsin 2; catalyst; Alzheimer's.

XX

OS Unidentified.

XX

PN WO200100663-A2.

XX



PD 04-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000WO-US017661.  
 XX  
 PR 28-JUN-1999; 99US-0141363P.  
 PR 30-NOV-1999; 99US-0168060P.  
 PR 25-JAN-2000; 2000US-0177836P.  
 PR 27-JAN-2000; 2000US-0178368P.  
 PR 08-JUN-2000; 2000US-0210292P.  
 XX  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX  
 PI Tang JJN, Lin X, Koelsch G;  
 XX  
 DR WPI; 2001-102885/11.  
 XX  
 PT Purified recombinant catalytically active memapsin 2, used to screen  
 PT inhibitors of it, which are used to treat and prevent Alzheimer's  
 PT disease.  
 XX  
 PS Claim 6; Page 11; 86pp; English.  
 XX  
 CC The present invention relates to a purified recombinant catalytically  
 CC active memapsin 2. The invention may be used for isolating inhibitors  
 CC which are used to treat or prevent Alzheimer's disease. The invention may  
 CC also be used to screen for individuals more genetically prone to develop  
 CC Alzheimer's disease  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 25

AAE02606

ID AAE02606 standard; peptide; 10 AA.

XX

AC AAE02606;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human wild-type APP beta-secretase substrate peptide, PHA-95812E.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;  
 KW Alzheimer's disease; antialzheimer's; aspartyl protease 2a; Asp2a;  
 KW beta-secretase.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

XX  
 PN WO200123533-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 22-SEP-2000; 2000WO-US026080.  
 XX  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Gurney M, Bienkowski MJ;  
 XX  
 DR WPI; 2001-290516/30.  
 XX  
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor  
 PT protein, useful for the treatment of Alzheimer's disease.  
 XX  
 PS Example 12; Page 85; 189pp; English.  
 XX  
 CC The present invention relates to enzymes for cleaving the alpha-  
 CC secretase site of the amyloid precursor protein (APP) and methods of  
 CC identifying those enzymes. The methods may be used to identify enzymes  
 CC that may be used to cleave the alpha-secretase cleavage site of the APP  
 CC protein. The enzymes may be used to treat or modulate the progress of  
 CC Alzheimer's disease. The present sequence is human wild-type amyloid  
 CC precursor protein (APP) beta-secretase specific substrate peptide, PHA-  
 CC 95812E. This peptide is used for assaying the beta-secretase activity of  
 CC human Aspartyl protease 2a (Asp2a) protein. The peptide is also used for  
 CC determining the relationship between Aspartyl protease 1 (Asp1) and APP  
 CC protein  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 26

AAB66574

ID AAB66574 standard; peptide; 10 AA.

XX

AC AAB66574;

XX

DT 12-APR-2001 (first entry)

XX

DE Synthetic peptide derived from APP beta-secretase site.

XX

KW Memapsin 2; nootropic; neuroprotective; amyloid precursor protein; APP;

KW memapsin 2 inhibitor; Alzheimer's disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200100665-A2.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 27-JUN-2000; 2000WO-US017742.  
 XX  
 PR 28-JUN-1999; 99US-0141363P.  
 PR 30-NOV-1999; 99US-0168060P.  
 PR 25-JAN-2000; 2000US-0177836P.  
 PR 27-JAN-2000; 2000US-0178368P.  
 PR 08-JUN-2000; 2000US-0210292P.  
 XX  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 PA (UNII ) UNIV ILLINOIS FOUND.  
 XX  
 PI Tang JJN, Hong L, Ghosh AK;  
 XX  
 DR WPI; 2001-137933/14.  
 XX  
 PT Novel memapsin 2 inhibitors which bind to active site of memapsin 2  
 PT having 2 catalytic aspartic residues and substrate binding cleft, used to  
 PT treat Alzheimer's disease by blocking amyloid precursor protein cleavage.  
 XX  
 PS Disclosure; Page 11; 86pp; English.  
 XX  
 CC The present sequence is given in a specification relating to an inhibitor  
 CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2  
 CC active site, which is defined by the presence of two catalytic aspartic  
 CC residues and a substrate binding cleft. The inhibitor is useful for the  
 CC treatment and diagnosis of Alzheimer's disease. It is useful in screens  
 CC for individuals with a genetic predisposition to Alzheimer's disease. The  
 CC inhibitor is useful as a reagent for specifically binding to memapsin 2  
 CC or memapsin 2 analogues and for aiding in memapsin 2 isolation,  
 CC purification and characterisation  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

RESULT 27  
 AAG62668  
 ID AAG62668 standard; peptide; 10 AA.  
 XX  
 AC AAG62668;  
 XX  
 DT 17-SEP-2001 (first entry)

XX  
 DE Beta-sheet breaker peptide inhibitor assay related peptide #3.  
 XX  
 KW Beta-sheet breaker peptide; protein conformational disease; amyloid;  
 KW Alzheimer's disease; FAF; Down' syndrome; amyloidosis disorder;  
 KW prion disease; prion associated neurodegenerative disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200134631-A2.  
 XX  
 PD 17-MAY-2001.  
 XX  
 PF 04-NOV-2000; 2000WO-US030416.  
 XX  
 PR 05-NOV-1999; 99US-0163911P.  
 XX  
 PA (AXON-) AXONYX INC.  
 XX  
 PI Soto-Jara C;  
 XX  
 DR WPI; 2001-408068/43.  
 XX  
 PT New peptide analogues and mimetics, useful by oral administration for the  
 PT treatment of Alzheimer's and prion disease by stabilization of the  
 PT conformation of amyloidogenic peptide.  
 XX  
 PS Example; Page 28; 48pp; English.  
 XX  
 CC The present invention relates to beta-sheet breaker peptide analogues  
 CC capable of inhibiting beta-pleated sheet formation in amyloid beta-  
 CC peptide. These are obtained by modification of a beta-sheet breaker  
 CC peptide. They can be used to reduce the formation of amyloid or amyloid-  
 CC like deposits involving abnormal folding into beta-sheet structures or  
 CC conformational change in prion Pr protein. They are thus useful in the  
 CC treatment of Alzheimer's disease, FAF, Down's syndrome, other amyloidosis  
 CC disorders, prion diseases such as kuru, Creutzfeldt-Jakob disease,  
 CC Gerstmann-Strausslet-Scheinker syndrome, prion associated human  
 CC neurodegenerative diseases, scrapie, spongiform encephalopathy,  
 CC transmissible mink encephalopathy and chronic wasting disease of mule  
 CC deer and elk. The present sequence is a peptide described in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 3 EVKMDAEF 10

RESULT 28  
 AAU06628  
 ID AAU06628 standard; peptide; 10 AA.

XX  
 AC AAU06628;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Asp2 recognition site from wild-type APP.  
 XX  
 KW Aspartyl protease; Asp2; beta-secretase; nootropic; neuroprotective;  
 KW amyloid protein precursor; APP; Alzheimer's disease; amyloid-beta; Abeta.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 5  
 FT /label= Asp2\_protease\_cleavage\_site  
 XX  
 PN WO200149098-A2.  
 XX  
 PD 12-JUL-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PR 09-MAY-2001; 2001WO-IB000798.  
 XX  
 PA (BIEN/) BIENKOWSKI M J.  
 PA (GURN/) GURNEY M E.  
 PA (HEIN/) HEINRIKSON R L.  
 PA (PARO/) PARODI L A.  
 PA (YANR/) YAN R.  
 XX  
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;  
 XX  
 DR WPI; 2001-502549/55.  
 XX  
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl  
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta  
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2  
 PT activity.  
 XX  
 PS Claim 127; Page 101; 185pp; English.  
 XX  
 CC The invention relates to a purified polypeptide comprising a fragment of  
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2  
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and  
 CC the fragment retain the beta-secretase activity of the mammalian Asp2  
 CC protein. The invention also details polynucleotides for the Asp proteins  
 CC and vectors expressing them, and a polypeptide (isoform of amyloid  
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or  
 CC its fragment containing an APP cleavage site recognizable by a mammalian  
 CC beta-secretase, and further comprising two lysine residues at the  
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP  
 CC fragment. Also included in the invention are methods of identifying  
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are  
 CC useful for treating Alzheimer's disease. APP is useful in methods for  
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-  
 CC beta (Abeta) peptide production. APP is also useful in designing  
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP

CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is  
CC associated with increased levels of Abeta processing is useful in assays  
CC relating the Alzheimer's research. The expression vector is useful for  
CC recombinantly expressing APP. Nucleic acids that hybridise to Asp  
CC oligonucleotides are useful as probes or primers. The probes are useful  
CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and  
CC Southern blots. The present sequence is a peptide substrate for Asp2  
CC corresponding to the wild-type APP beta-secretase site

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 2 EVKMDAEF 9

#### RESULT 29

ABB06426

ID ABB06426 standard; peptide; 10 AA.

XX

AC ABB06426;

XX

DT 31-MAY-2002 (first entry)

XX

DE Human APP beta-secretase cleavage sequence SEQ ID NO:20.

XX

KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;  
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;  
KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200206306-A2.

XX

PD 24-JAN-2002.

XX

PF 19-JUL-2001; 2001WO-US023035.

XX

PR 19-JUL-2000; 2000US-0219795P.

PR 12-MAR-2001; 2001US-0275251P.

XX

PA (PHAA ) PHARMACIA & UPJOHN CO.

XX

PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;  
PI Heinrikson RL;

XX

DR WPI; 2002-216995/27.

XX

PT Novel substrates for human aspartyl protease useful for identifying  
PT modulators of beta secretase activity of aspartyl protease for treating  
PT Alzheimer's disease.

XX

PS Claim 18; Page 126; 188pp; English.



XX  
 CC The present invention describes an isolated peptide (I) comprising a  
 CC sequence of at least four amino acids, where the peptide is a substrate  
 CC for conducting aspartyl protease assays. (I) has neuroprotective and  
 CC nootropic activities, and can be used as an inhibitor of beta-secretase  
 CC activity. A beta-secretase modulator from the present invention can be  
 CC used for inhibiting beta-secretase activity in vivo, and in the  
 CC manufacture of a medicament for the treatment of Alzheimer's disease.  
 CC Pharmaceutical compositions from the present invention can be used for  
 CC treating a disease or condition characterised by an abnormal beta-  
 CC secretase activity. (I) is useful for identifying agents that modulate  
 CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as  
 CC a core structure to construct derivatives. ABL49914 to ABL49925 and  
 CC ABB06409 to ABB06593 represent sequences used in the exemplification of  
 CC the present invention

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 30

ABG78375

ID ABG78375 standard; peptide; 10 AA.

XX

AC ABG78375;

XX

DT 15-NOV-2002 (first entry)

XX

DE Human beta amyloid precursor protein beta secretase site #1.

XX

KW Human; memapsin 2; aspartic protease; beta secretase;

KW degenerative disease; Alzheimer's disease; amyloid precursor protein;

KW APP; neuroprotective; nootropic; inhibitor; cleavage site;

KW substrate side-chain preference.

XX

OS Homo sapiens.

XX

PN WO200253594-A2.

XX

PD 11-JUL-2002.

XX

PF 28-DEC-2001; 2001WO-US050826.

XX

PR 28-DEC-2000; 2000US-0258705P.

PR 14-MAR-2001; 2001US-0275756P.

XX

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA (UNII ) UNIV ILLINOIS FOUND.

XX

PI Tang JJN, Koelsch G, Ghosh AK;

XX  
 DR WPI; 2002-619088/66.  
 XX  
 PT New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's  
 PT disease.  
 XX  
 PS Disclosure; Page 23; 74pp; English.  
 XX  
 CC The invention relates to an inhibitor of catalytically active memapsin 2  
 CC (an aspartic protease which can cleave at beta secretase sites), which  
 CC binds to the active site of memapsin 2 defined by the presence of two  
 CC catalytic aspartic residues and substrate binding cleft. Also included is  
 CC a method of determination of the substrate side-chain preference in  
 CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2  
 CC substrates with memapsin 2, and determining the sub-site preference of  
 CC memapsin 2 by determining relative initial hydrolysis rates of the  
 CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial  
 CC library of memapsin 2 inhibitors containing a base sequence taken from  
 CC OM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of  
 CC inhibitors with memapsin 2 which binds to several inhibitors to generate  
 CC several bound memapsin 2, and detecting the bound memapsin 2 with an  
 CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated  
 CC secondary antibody. The inhibitors may be used in the manufacture of a  
 CC medicament for the treatment of Alzheimer's disease since memapsin 2 may  
 CC be involved in the cleavage of amyloid precursor protein (APP), and for  
 CC determining the substrate side-chain preference in memapsin 2 sub-sites.  
 CC The present sequence represents a beta secretase cleavage site used to  
 CC determine the substrate specificity of human memapsin 2  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 31

ABB78615

ID ABB78615 standard; peptide; 10 AA.

XX

AC ABB78615;

XX

DT 16-JUL-2002 (first entry)

XX

DE Beta-secretase specific substrate PHA-95812E SEQ ID NO:64.

XX

KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.

XX

OS Synthetic.

XX

PN GB2367060-A.

XX

PD 27-MAR-2002.

XX  
 PF 29-OCT-2001; 2001GB-00025934.  
 XX  
 PR 23-SEP-1999; 99US-00404133.  
 PR 23-SEP-1999; 99US-0155493P.  
 PR 23-SEP-1999; 99WO-US020881.  
 PR 13-OCT-1999; 99US-00416901.  
 PR 06-DEC-1999; 99US-0169232P.  
 PR 22-SEP-2000; 2000GB-00023315.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 PI Bienkowski MJ, Gurney M;  
 XX  
 DR WPI; 2002-397167/43.  
 XX  
 PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl  
 PT protease activity, e.g. for the diagnosis of Alzheimer's disease.  
 XX  
 PS Example 15; Page 92; 182pp; English.  
 XX  
 CC The present invention describes a human aspartyl protease 1 (hu-Asp1)  
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,  
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-  
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1  
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with  
 CC (I) under acidic conditions; and (b) determining the level of hu-Asp1  
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a  
 CC nucleotide sequence that hybridises under stringent conditions to the non  
 CC -coding strand complementary to a defined 1804 nucleotide sequence (see  
 CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1  
 CC proteolytic activity and lacks nucleotides encoding a transmembrane  
 CC domain); (3) a purified polynucleotide (III') comprising a sequence that  
 CC hybridises under stringent conditions to (III) (the nucleotide sequence  
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding  
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)  
 CC comprising (III) or (III'); and (5) a host cell (V) transformed or  
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease  
 CC substrate (I) may be used as an enzyme substrate in assays to detect  
 CC aspartyl protease activity, (II) and therefore diagnose diseases  
 CC associated with aberrant hu-Asp1 expression and activity such as  
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while  
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present  
 CC sequence represents a beta-secretase specific substrate peptide which is  
 CC used in an example from the present invention  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

RESULT 32  
 AAU99490  
 ID AAU99490 standard; peptide; 10 AA.  
 XX  
 AC AAU99490;  
 XX  
 DT 07-OCT-2002 (first entry)  
 XX  
 DE Peptide #1 used as substrate for human memapsin 2.  
 XX  
 KW Human; memapsin 2; beta secretase; aspartic protease; APP;  
 KW beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;  
 KW neuroprotective; nootropic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN US2002049303-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 28-FEB-2001; 2001US-00796264.  
 XX  
 PR 28-JUN-1999; 99US-0141363P.  
 PR 30-NOV-1999; 99US-0168060P.  
 PR 25-JAN-2000; 2000US-0177836P.  
 PR 27-JAN-2000; 2000US-0178368P.  
 PR 27-JUN-2000; 2000US-00604608.  
 XX  
 PA (TANG/) TANG J J N.  
 PA (LINX/) LIN X.  
 PA (KOEL/) KOELSCH G.  
 PA (HONG/) HONG L.  
 XX  
 PI Tang JJN, Lin X, Koelsch G, Hong L;  
 XX  
 DR WPI; 2002-507280/54.  
 XX  
 PT New recombinant catalytically active memapsin 2, useful to screen for  
 PT inhibitors of memapsin 2 which can be used to prevent and treat  
 PT Alzheimer's disease.  
 XX  
 PS Claim 6; Page 30; 44pp; English.  
 XX  
 CC The present invention relates to methods for the production of purified,  
 CC recombinant catalytically active, memapsin 2 (beta secretase). Memapsin  
 CC 2, a member of the aspartic protease family, cleaves beta-amyloid  
 CC precursor protein (APP) found in amyloid plaques. The recombinant  
 CC memapsin 2 is useful for identifying inhibitors of memapsin 2 in the  
 CC design of drugs for the treatment and/or prevention of Alzheimer's  
 CC disease. The recombinant memapsin 2 can be used to immunise against  
 CC Alzheimer's disease. The present sequence represents a peptide used as a  
 CC substrate for human memapsin 2  
 XX  
 SQ Sequence 10 AA;

Query Match

100.0%; Score 8; DB 5; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
      |||||||  
Db 2 EVKMDAEF 9

RESULT 33

ABG30940

ID ABG30940 standard; peptide; 10 AA.

XX

AC ABG30940;

XX

DT 21-OCT-2002 (first entry)

XX

DE Nogo/BACE method cleavage peptide #1.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;  
KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
KW tissue hypertrophy; central nervous system; axon regeneration;  
KW Nogo-associated disease; metastasis; cleavage peptide.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Cleavage-site 5. .6

FT /note= "Beta-secretase cleavage site"

XX

PN WO200257483-A2.

XX

PD 25-JUL-2002.

XX

PF 18-JAN-2002; 2002WO-GB000228.

XX

PR 18-JAN-2001; 2001GB-00001312.

XX

PA (GLAX ) GLAXO GROUP LTD.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.

XX

PS Disclosure; Page 14; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating

CC acute neuronal injuries, such as spinal or head injury, stroke,  
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
 CC hypertrophy) of the central nervous system. The BACE polypeptide is  
 CC useful in screening methods to identify agents that may act as modulators  
 CC of BACE activity and in particular agents that may be useful in treating  
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
 CC and the polynucleotide encoding the BACE polypeptide are useful in  
 CC manufacturing a medicament for the treatment or prevention of disorders  
 CC responsive to the modulation of Nogo activity, in alleviating the  
 CC symptoms or improving the condition of a patient suffering from this  
 CC disorder, in axon regeneration, or in preventing metastasis or spreading  
 CC of a cancer. The polynucleotide may also be an essential component in  
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
 CC techniques. The present amino acid sequence represents a cleavage peptide  
 CC that was used in the methods of the invention

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

#### RESULT 34

ABG76103

ID ABG76103 standard; peptide; 10 AA.

XX

AC ABG76103;

XX

DT 01-MAY-2003 (first entry)

XX

DE Amyloid precursor protein derived substrate peptide.

XX

KW Human; memapsin 2; beta-secretase; beta-amyloid precursor protein;  
 KW beta-amyloid peptide; Alzheimer's disease; nootropic; neuroprotective;  
 KW substrate.

XX

OS Homo sapiens.

XX

PN US2002164760-A1.

XX

PD 07-NOV-2002.

XX

PF 28-FEB-2001; 2001US-00795903.

XX

PR 28-JUN-1999; 99US-0141363P.

PR 30-NOV-1999; 99US-0168060P.

PR 25-JAN-2000; 2000US-0177836P.

PR 27-JAN-2000; 2000US-0178368P.

PR 08-JUN-2000; 2000US-0210292P.

PR 27-JUN-2000; 2000US-00604608.

XX  
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
XX  
PI Lin X, Koelsch G, Tang JJN;  
XX  
DR WPI; 2003-255218/25.  
XX  
PT New purified recombinant catalytically active memapsin 2 (beta-  
PT secretase), useful for designing and screening of specific inhibitors for  
PT the diagnosis, prevention and/or treatment of Alzheimer's disease.  
XX  
PS Claim 6; Page 4; 44pp; English.  
XX  
CC The invention relates to a purified recombinant catalytically active  
CC memapsin 2, a beta-secretase which produces the beta-amyloid peptide from  
CC the beta amyloid precursor protein. Also included are producing the above  
CC memapsin 2 (comprising refolding the recombinant memapsin 2 under  
CC conditions which dissociate and then slowly refold the enzyme into a  
CC catalytically active form), isolating inhibitors of cleavage by memapsin  
CC 2 (comprising adding to one or more potential inhibitors the memapsin 2  
CC and a substrate for memapsin 2 and screening for decreased cleavage of  
CC the substrate by the inhibitors), designing or obtaining inhibitors of  
CC the memapsin 2 (comprising modelling an inhibitor based on the  
CC crystallisation coordinates of memapsin 2 or the parameters given in the  
CC specification), a database comprising binding properties and chemical  
CC structures of compounds designed or screened by the method above and  
CC treating or preventing Alzheimer's disease (comprising administering to a  
CC patient an inhibitor of memapsin 2 which binds to the active site of the  
CC memapsin 2 defined by the presence of 2 catalytic aspartic residues and  
CC substrate binding cleft or immunising an individual with the above  
CC memapsin 2 to elicit an amount of antibodies to reduce the cleavage by  
CC endogenous memapsin 2). The memapsin 2 is useful in designing and  
CC screening of specific inhibitors for the diagnosis, prevention and/or  
CC treatment of Alzheimer's disease. The present sequence represents an  
CC amyloid precursor protein substrate peptide which is cleaved by memapsin  
CC 2  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

# RESULT 35

ABR61933

ID ABR61933 standard; peptide; 10 AA.

XX

AC ABR61933;

XX

DT 12-SEP-2003 (first entry)

XX

DE Human APP beta-secretase cleavage site fragment.



XX  
 KW Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;  
 KW beta-amyloid protein; Alzheimer's disease; amyloid precursor protein;  
 KW APP; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003039454-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 23-OCT-2002; 2002WO-US034324.  
 XX  
 PR 23-OCT-2001; 2001US-0335952P.  
 PR 27-NOV-2001; 2001US-0333545P.  
 PR 14-JAN-2002; 2002US-0348464P.  
 PR 14-JAN-2002; 2002US-0348615P.  
 PR 20-JUN-2002; 2002US-0390804P.  
 PR 19-JUL-2002; 2002US-0397557P.  
 PR 19-JUL-2002; 2002US-0397619P.  
 XX  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 PA (UNII ) UNIV ILLINOIS FOUND.  
 XX  
 PI Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;  
 PI Turner RT;  
 XX  
 DR WPI; 2003-541410/51.  
 XX  
 PT New peptide compounds are memapsin beta secretase inhibitors used for  
 PT treating Alzheimer's disease.  
 XX  
 PS Claim 90; Page 204; 407pp; English.  
 XX  
 CC The invention relates to peptide compounds of specified formula. The  
 CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative  
 CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid  
 CC protein. The compounds can be used for treating Alzheimer's disease. The  
 CC present sequence represents a human amyloid precursor protein (APP) beta-  
 CC secretase cleavage site fragment  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

RESULT 36  
 ADA74819  
 ID ADA74819 standard; peptide; 10 AA.  
 XX  
 AC ADA74819;

XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human amyloid precursor protein beta-secretase site-derived peptide 1.  
 XX  
 KW memapsin 2; beta-secretase; amyloid precursor protein; APP;  
 KW aspartic proteinase 2; ASP2; nootropic; neuroprotective;  
 KW Alzheimer's disease; human.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 5. .6  
 FT /note= "Beta-secretase cleavage site"  
 XX  
 PN US6545127-B1.  
 XX  
 PD 08-APR-2003.  
 XX  
 PF 27-JUN-2000; 2000US-00604608.  
 XX  
 PR 28-JUN-1999; 99US-0141363P.  
 PR 30-NOV-1999; 99US-0168060P.  
 PR 25-JAN-2000; 2000US-0177836P.  
 PR 27-JAN-2000; 2000US-0178368P.  
 PR 08-JUN-2000; 2000US-0210292P.  
 XX  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX  
 PI Tang JJN, Lin X, Koelsch G, Hong L;  
 XX  
 DR WPI; 2003-566587/53.  
 XX  
 PT Novel memapsin 2 protein that cleaves a beta-secretase site of an amyloid  
 PT precursor protein is useful in the design and screening of specific  
 PT inhibitors for treating and preventing Alzheimer's disease.  
 XX  
 PS Claim 17; Col 7; 44pp; English.  
 XX  
 CC The invention relates to a novel method which comprises the production of  
 CC purified, catalytically active, recombinant memapsin 2 (beta-secretase)  
 CC protein where the memapsin protein is expressed in a bacterial cell and  
 CC cleaves the beta-secretase site of an amyloid precursor protein (APP).  
 CC Memapsin 2, also known as aspartic proteinase 2 (ASP2), belongs to the  
 CC aspartic protease family and demonstrates nootropic and neuroprotective  
 CC activities. The protein of the invention may be useful in the design and  
 CC screening of specific inhibitors which are useful in treating and  
 CC preventing Alzheimer's disease. The current sequence is that of the human  
 CC APP beta-secretase site-derived peptide 1 of the invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | |  
Db 2 EVKMDAEF 9

RESULT 37

ADB75175

ID ADB75175 standard; peptide; 10 AA.

XX

AC ADB75175;

XX

DT 04-DEC-2003 (first entry)

XX

DE Amyloid beta peptide negative control spanning peptide.

XX

KW antibody; amyloid beta peptide; amyloid beta; nootropic; neuroprotective;

KW antibody therapy; Alzheimer's disease; mild cognitive impairment;

KW cerebral amyloid angiopathy; congiphylic angiopathy; Down's syndrome;

KW inclusion body myositis; neurotoxicity; beta amyloid precursor protein;

KW APP; human.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= acetylated

XX

PN WO2003074081-A1.

XX

PD 12-SEP-2003.

XX

PF 21-OCT-2002; 2002WO-US031590.

XX

PR 28-FEB-2002; 2002US-00084380.

XX

PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

XX

PI Chain DG;

XX

DR WPI; 2003-731651/69.

XX

PT New antibody that is targeted to amyloid beta peptide, or its fragment,

PT useful for treating a subject having Alzheimer's disease, or a disease or

PT disorder characterized by amyloid beta deposition, e.g. cognitive

PT impairment or dementia.

XX

PS Example 2; Page 29; 63pp; English.

XX

CC The present invention describes an antibody that is targeted to amyloid

CC beta peptide, or its fragment. Also described: (1) an antibody that is

CC free-end specific and is targeted to: (a) the free N-terminus of amyloid

CC beta-peptide; (b) the free N-terminus of amyloid beta-peptide, where the

CC first amino acid of amyloid beta-peptide is aspartate; (c) the free N-

CC terminus of N- and/or C-terminus-truncated amyloid beta-peptide fragment;

CC (d) the free C-terminus of the amyloid beta-peptide Abetal-39, Abetal-40,

CC Abetal-41 or Abetal-43; or (e) to the free C-terminus of N- and/or C-

CC terminus-truncated amyloid beta-peptide fragment; (2) a single chain or  
 CC artificial antibody that is free-end specific and is targeted to the free  
 CC C-terminus of the amyloid beta-peptide Abeta1-42; and (3) a  
 CC pharmaceutical composition comprising the antibody, and a carrier. The  
 CC antibody targeted to amyloid beta peptide has nootropic and  
 CC neuroprotective activities, and can be used in antibody therapy. The  
 CC antibody or its fragment is useful for manufacturing a medicament for  
 CC treating a subject having Alzheimer's disease, or a disease or disorder  
 CC characterised by amyloid beta deposition (e.g. mild cognitive impairment,  
 CC cerebral amyloid angiopathy or congophilic angiopathy, Alzheimer's  
 CC disease associated with Down's syndrome, or inclusion body myositis), or  
 CC for delaying, inhibiting or suppressing accumulation of amyloid beta  
 CC peptide, or the neurotoxicity of amyloid beta peptide or its fragment.  
 CC Amyloid beta peptides are derived from beta amyloid precursor protein  
 CC (APP). The present sequence represents an amyloid beta peptide negative  
 CC control spanning peptide, which is used in an example from the present  
 CC invention.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 8; DB 7; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0026;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8

|||||||

Db 1 EVKMDAEF 8

RESULT 38

AAB97468

ID AAB97468 standard; protein; 11 AA.

XX

AC AAB97468;

XX

DT 03-AUG-2001 (first entry)

XX

DE Asp2 substrate wild-type beta-site peptide sequence.

XX

KW Asp2; endocrepain 2; memapsin 2; beta-amyloid protein;

KW Alzheimer's disease; cortical Lewy body disease; Parkinson's disease;

KW Asp2 inhibitor.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "optionally bound to maltose binding protein"

XX

PN WO200129563-A1.

XX

PD 26-APR-2001.

XX

PF 19-OCT-2000; 2000WO-GB004039.

XX

PR 21-OCT-1999; 99GB-00024957.

XX  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Christie G, Hussain I, Powell DJ;  
XX  
DR WPI; 2001-300381/31.  
XX  
PT Screening for inhibitors of Asp 2 mediated polypeptide cleavage comprises  
PT measuring substrate cleavage or ligand binding with a system comprising  
PT Asp 2 and a substrate or labelled ligand in the presence or absence of a  
PT test compound.  
XX  
PS Disclosure; Page 3; 34pp; English.  
XX  
CC The present invention describes a method of screening for compounds which  
CC inhibit Asp2 (also known as memapsin 2 and endocrepain 2) mediated  
CC cleavage of a protein substrate, involving measuring the extent of  
CC cleavage of the substrate in the presence and absence of the test  
CC compound. Asp2 is thought to be involved in the cleavage of amyloid  
CC precursor protein which is excised to produce beta-amyloid. Beta-amyloid  
CC is involved in the pathogenesis of Alzheimer's disease, Parkinson's  
CC disease, cortical Lewy body disease and vascular and cerebrovascular  
CC diseases, and Asp2 inhibitors could be useful in their treatment. The  
CC present sequence is an example of an Asp2 substrate  
XX  
SQ Sequence 11 AA;

Query Match 100.0%; Score 8; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
| | | | | | | |  
Db 3 EVKMDAEF 10

# RESULT 39

AAB75144

ID AAB75144 standard; peptide; 11 AA.

XX

AC AAB75144;

XX

DT 08-AUG-2001 (first entry)

XX

DE Asp 1 substrate sequence SEQ ID NO:3.

XX

KW Amyloid precursor protein; APP; Asp 1; endocrepain 1; inhibition;  
KW transmembrane aspartyl proteinase; APP Swedish variant; nootropic;  
KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;  
KW beta amyloid protein-related disease; antialzheimer.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminally attached to maltose binding protein

FT (MBP) "  
 XX  
 PN WO200131054-A1.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 19-OCT-2000; 2000WO-GB004028.  
 XX  
 PR 22-OCT-1999; 99GB-00025136.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Christie G, Hussain I, Powell DJ;  
 XX  
 DR WPI; 2001-328654/34.  
 XX  
 PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or  
 PT preventing beta-amyloid protein-related disease, comprises measuring the  
 PT extent of substrate cleavage in a reaction system containing Asp 1 and a  
 PT substrate.  
 XX  
 PS Disclosure; Page 3; 31pp; English.  
 XX  
 CC The present invention describes a method of screening for compounds which  
 CC inhibit Asp 1-mediated cleavage of a polypeptide or protein substrate.  
 CC The method comprises providing a reaction system comprising Asp 1 and  
 CC substrate, and measuring the extent of cleavage of the substrate in the  
 CC presence of test compound compared with that in the presence of the test  
 CC compound. Also described are: (1) a method of screening for compounds  
 CC which inhibit Asp 1 mediated cleavage of a polypeptide or protein  
 CC substrate comprising providing a reaction system comprising Asp 1 and a  
 CC labeled active site ligand, and measuring the extent of binding of the  
 CC labeled ligand in the presence of test compound compared with that in the  
 CC presence of the test compound; (2) a compound identified by the method;  
 CC (3) a pharmaceutical composition comprising the compound of (2) and a  
 CC carrier; (4) a method of inhibiting Asp 1 modulated amyloid precursor  
 CC protein (APP) cleavage, or treating or prophylaxis of beta-amyloid  
 CC protein-related disease, comprising administering to a patient a compound  
 CC of (2); (5) a compound which is an inhibitor of Asp 1 modulated APP  
 CC cleavage; and (6) a method for treating or prophylaxis of beta-amyloid  
 CC protein-related disease comprising administering a compound of (2) or  
 CC (5). The compound which inhibits Asp 1 mediated cleavage of a polypeptide  
 CC or protein is useful in therapy, in the preparation of a medicament for  
 CC inhibiting Asp 1-modulated APP cleavage and for the treatment or  
 CC prophylaxis of beta-amyloid protein-related disease, including  
 CC Alzheimer's disease. The present sequence represents an Asp 1 substrate  
 CC sequence which is given in the exemplification of the present invention  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 8; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0028;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||

## RESULT 40

AAB75143

ID AAB75143 standard; peptide; 11 AA.

XX

AC AAB75143;

XX

DT 08-AUG-2001 (first entry)

XX

DE APP beta-secretase cleavage site spanning peptide SEQ ID NO:1.

XX

KW Amyloid precursor protein; APP; Asp 1; endocrepisin 1; inhibition;

KW transmembrane aspartyl proteinase; APP Swedish variant; nootropic;

KW neuroprotective; beta-secretase cleavage site; Alzheimer's disease;

KW beta amyloid protein-related disease; antialzheimer.

XX

OS Homo sapiens.

XX

PN WO200131054-A1.

XX

PD 03-MAY-2001.

XX

PF 19-OCT-2000; 2000WO-GB004028.

XX

PR 22-OCT-1999; 99GB-00025136.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Christie G, Hussain I, Powell DJ;

XX

DR WPI; 2001-328654/34.

XX

PT Identifying inhibitors of Asp 1-mediated cleavage, for treating or  
PT preventing beta-amyloid protein-related disease, comprises measuring the  
PT extent of substrate cleavage in a reaction system containing Asp 1 and a  
PT substrate.

XX

PS Disclosure; Page 3; 3lpp; English.

XX

CC The present invention describes a method of screening for compounds which  
CC inhibit Asp 1-mediated cleavage of a polypeptide or protein substrate.  
CC The method comprises providing a reaction system comprising Asp 1 and  
CC substrate, and measuring the extent of cleavage of the substrate in the  
CC presence of test compound compared with that in the presence of the test  
CC compound. Also described are: (1) a method of screening for compounds  
CC which inhibit Asp 1 mediated cleavage of a polypeptide or protein  
CC substrate comprising providing a reaction system comprising Asp 1 and a  
CC labeled active site ligand, and measuring the extent of binding of the  
CC labeled ligand in the presence of test compound compared with that in the  
CC presence of the test compound; (2) a compound identified by the method;  
CC (3) a pharmaceutical composition comprising the compound of (2) and a  
CC carrier; (4) a method of inhibiting Asp 1 modulated amyloid precursor  
CC protein (APP) cleavage, or treating or prophylaxis of beta-amyloid  
CC protein-related disease, comprising administering to a patient a compound



CC of (2); (5) a compound which is an inhibitor of Asp 1 modulated APP  
CC cleavage; and (6) a method for treating or prophylaxis of beta-amyloid  
CC protein-related disease comprising administering a compound of (2) or  
CC (5). The compound which inhibits Asp 1 mediated cleavage of a polypeptide  
CC or protein is useful in therapy, in the preparation of a medicament for  
CC inhibiting Asp 1-modulated APP cleavage and for the treatment or  
CC prophylaxis of beta-amyloid protein-related disease, including  
CC Alzheimer's disease. The present sequence represents an APP beta-  
CC secretase cleavage site spanning peptide which can be used as a substrate  
CC in the method of the invention

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 8; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 3 EVKMDAEF 10

Search completed: March 26, 2004, 15:32:47

Job time : 70.5 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:37 ; Search time 16.5 Seconds  
 (without alignments)  
 25.031 Million cell updates/sec

Title: US-09-668-314C-70  
 Perfect score: 8  
 Sequence: 1 EVKMDAEF 8

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents\_AA:\*  
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 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	8	100.0	8	4	US-09-548-372D-67	Sequence 67, Appl
2	8	100.0	8	4	US-09-548-367D-67	Sequence 67, Appl
3	8	100.0	8	4	US-09-551-853D-67	Sequence 67, Appl
4	8	100.0	9	3	US-08-802-981-221	Sequence 221, App
5	8	100.0	9	4	US-09-294-987-6	Sequence 6, Appli
6	8	100.0	9	4	US-09-724-566A-82	Sequence 82, Appl
7	8	100.0	10	2	US-08-025-321C-1	Sequence 1, Appli
8	8	100.0	10	4	US-09-548-372D-64	Sequence 64, Appl
9	8	100.0	10	4	US-09-548-367D-64	Sequence 64, Appl
10	8	100.0	10	4	US-09-551-853D-64	Sequence 64, Appl
11	8	100.0	10	4	US-09-604-608-4	Sequence 4, Appli

12	8	100.0	11	5	PCT-US94-07043A-7	Sequence 7, Appli
13	8	100.0	12	5	PCT-US94-07043A-2	Sequence 2, Appli
14	8	100.0	15	4	US-09-548-372D-71	Sequence 71, Appl
15	8	100.0	15	4	US-09-548-367D-71	Sequence 71, Appl
16	8	100.0	15	4	US-09-551-853D-71	Sequence 71, Appl
17	8	100.0	16	5	PCT-US94-07043A-1	Sequence 1, Appli
18	8	100.0	21	3	US-08-802-981-114	Sequence 114, App
19	8	100.0	27	1	US-08-141-324-11	Sequence 11, Appl
20	8	100.0	27	1	US-08-541-902-11	Sequence 11, Appl
21	8	100.0	45	1	US-08-462-859A-5	Sequence 5, Appli
22	8	100.0	45	1	US-08-123-659A-5	Sequence 5, Appli
23	8	100.0	45	1	US-08-464-247A-5	Sequence 5, Appli
24	8	100.0	45	1	US-08-464-248A-5	Sequence 5, Appli
25	8	100.0	58	1	US-08-371-930-25	Sequence 25, Appl
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112	8	100.0	753	4	US-09-548-367D-61	Sequence 61, Appl
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130	7	87.5	18	2	US-08-149-975A-3	Sequence 3, Appli
131	7	87.5	48	4	US-09-560-883-1	Sequence 1, Appli
132	7	87.5	53	3	US-09-173-887-5	Sequence 5, Appli
133	7	87.5	53	4	US-09-797-543-5	Sequence 5, Appli
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135	5	62.5	5	2	US-08-422-333-7	Sequence 7, Appli
136	5	62.5	5	2	US-08-659-984A-13	Sequence 13, Appl
137	5	62.5	5	3	US-08-660-531-13	Sequence 13, Appl
138	5	62.5	5	4	US-09-054-334-1	Sequence 1, Appli
139	5	62.5	5	4	US-09-724-566A-54	Sequence 54, Appl
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165	5	62.5	331	4	US-09-531-056A-12	Sequence 12, Appl
166	5	62.5	377	4	US-09-198-452A-1000	Sequence 1000, Ap
167	5	62.5	408	4	US-09-328-352-6014	Sequence 6014, Ap
168	5	62.5	409	4	US-09-198-452A-554	Sequence 554, App
169	5	62.5	429	4	US-09-252-991A-31213	Sequence 31213, A
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174	5	62.5	467	4	US-09-002-361-3	Sequence 3, Appli
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176	5	62.5	488	1	US-08-554-659-4	Sequence 4, Appli
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181	5	62.5	631	4	US-09-107-532A-3902	Sequence 3902, Ap
182	5	62.5	672	4	US-09-540-236-2659	Sequence 2659, Ap

183	5	62.5	800	4	US-09-107-532A-4095	Sequence 4095, Ap
184	5	62.5	882	4	US-09-328-352-5232	Sequence 5232, Ap
185	5	62.5	907	3	US-08-938-830-26	Sequence 26, Appl
186	5	62.5	907	3	US-09-020-222-26	Sequence 26, Appl
187	5	62.5	915	4	US-09-252-991A-22344	Sequence 22344, A
188	5	62.5	1221	4	US-09-107-532A-3959	Sequence 3959, Ap
189	5	62.5	1381	4	US-09-808-701A-25	Sequence 25, Appl
190	4	50.0	4	2	US-08-025-321C-12	Sequence 12, Appl
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192	4	50.0	4	4	US-09-294-987-2	Sequence 2, Appli
193	4	50.0	4	4	US-09-054-334-5	Sequence 5, Appli
194	4	50.0	4	4	US-09-513-783A-92	Sequence 92, Appl
195	4	50.0	4	4	US-09-797-543-1	Sequence 1, Appli
196	4	50.0	4	4	US-09-724-566A-103	Sequence 103, App
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#### ALIGNMENTS

#### RESULT 1

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; Patent No. 6420534

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; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

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Query Match 100.0%; Score 8; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 1 EVKMDAEF 8

RESULT 2

US-09-548-367D-67

; Sequence 67, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 67

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Peptide

US-09-548-367D-67

Query Match 100.0%; Score 8; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
|||||||  
Db 1 EVKMDAEF 8

RESULT 3

US-09-551-853D-67

; Sequence 67, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D



; CURRENT FILING DATE: 2000-04-18  
 ; PRIOR APPLICATION NUMBER: US 60/155,493  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: US 09/404,133  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881  
 ; PRIOR FILING DATE: 1999-09-23  
 ; PRIOR APPLICATION NUMBER: US 60/101,594  
 ; PRIOR FILING DATE: 1998-09-24  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 67  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Peptide  
 US-09-551-853D-67

Query Match 100.0%; Score 8; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 1 EVKMDAEF 8

# RESULT 4

US-08-802-981-221

; Sequence 221, Application US/08802981  
 ; Patent No. 6037137

## ; GENERAL INFORMATION:

; APPLICANT: Komoriya, Akira  
 ; APPLICANT: Packard, Beverly S.  
 ; TITLE OF INVENTION: Compositions for the Detection of Enzyme  
 ; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use  
 Thereof

; NUMBER OF SEQUENCES: 231  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/802,981  
 ; FILING DATE: 20-FEB-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hunter, Tom

```

;   REGISTRATION NUMBER:  38,498
;   REFERENCE/DOCKET NUMBER:  016865-000300US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 576-0200
;   TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  221:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  9 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-802-981-221

```

```

Query Match          100.0%;  Score 8;  DB 3;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 3e+05;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 EVKMDAEF 8
             |||||
Db          2 EVKMDAEF 9

```

RESULT 5

```

US-09-294-987-6
; Sequence 6, Application US/09294987
; Patent No. 6313268
; GENERAL INFORMATION:
; APPLICANT:  Hook, Vivian Y.H.
; TITLE OF INVENTION:  SECRETASES RELATED TO ALZHEIMER'S DEMENTIA
; FILE REFERENCE:  P-AS 3515
; CURRENT APPLICATION NUMBER:  US/09/294,987
; CURRENT FILING DATE:  1999-04-20
; PRIOR APPLICATION NUMBER:  US 09/173,887
; PRIOR FILING DATE:  1998-10-16
; NUMBER OF SEQ ID NOS:  6
; SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH:  9
;   TYPE:  PRT
;   ORGANISM:  mammalian
US-09-294-987-6

```

```

Query Match          100.0%;  Score 8;  DB 4;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 3e+05;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 EVKMDAEF 8
             |||||
Db          2 EVKMDAEF 9

```

RESULT 6

```

US-09-724-566A-82
; Sequence 82, Application US/09724566A
; Patent No. 6627739
; GENERAL INFORMATION:

```

; APPLICANT: Anderson, John P.  
 ; APPLICANT: Basi, Gurigbal  
 ; APPLICANT: Doane, Minh Tam  
 ; APPLICANT: Frigon, No. 6627739mand  
 ; APPLICANT: John, Varghese  
 ; APPLICANT: Power, Michael  
 ; APPLICANT: Sinha, Sukanto  
 ; APPLICANT: Tatsuno, Gwen  
 ; APPLICANT: Tung, Jay  
 ; APPLICANT: Wang, Shuwen  
 ; APPLICANT: McConlogue, Lisa  
 ; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and  
 ; TITLE OF INVENTION: Methods  
 ; FILE REFERENCE: 228-US-NEWC2  
 ; CURRENT APPLICATION NUMBER: US/09/724,566A  
 ; CURRENT FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: US 09/501,708  
 ; PRIOR FILING DATE: 2000-02-10  
 ; PRIOR APPLICATION NUMBER: 60/119,571  
 ; PRIOR FILING DATE: 1999-02-10  
 ; PRIOR APPLICATION NUMBER: 60/139,172  
 ; PRIOR FILING DATE: 1999-06-15  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 82  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: APP fragment P5-P4' wt  
 US-09-724-566A-82

Query Match 100.0%; Score 8; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 7

US-08-025-321C-1

; Sequence 1, Application US/08025321C

; Patent No. 5849560

; GENERAL INFORMATION:

; APPLICANT: Abraham Ph.D., Carmela R.

; TITLE OF INVENTION: PROTEASES CAUSING ABNORMAL DEGREDAATION

; TITLE OF INVENTION: OF AMYLOID BETA-PROTEIN PRECURSOR

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Choate, Hall & Stewart

; STREET: 53 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/025,321C
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0079571-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 248 5000
; TELEFAX: 617 248 4000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-025-321C-1

```

```

Query Match          100.0%; Score 8; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      3 EVKMDAEF 10

```

RESULT 8

US-09-548-372D-64

; Sequence 64, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64

; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-548-372D-64

Query Match 100.0%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 9

US-09-548-367D-64

; Sequence 64, Application US/09548367D  
; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-548-367D-64

Query Match 100.0%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 10

US-09-551-853D-64

```

; Sequence 64, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-551-853D-64

```

```

Query Match          100.0%; Score 8; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      2 EVKMDAEF 9

```

# RESULT 11

US-09-604-608-4

```

; Sequence 4, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368

```

; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/210,292  
; PRIOR FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-604-608-4

Query Match 100.0%; Score 8; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 12

PCT-US94-07043A-7

; Sequence 7, Application PC/TUS9407043A

; GENERAL INFORMATION:

; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC  
; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Miles Inc.  
; STREET: 400 Morgan Lane  
; CITY: West Haven  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06516

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
; COMPUTER: Sharp PC 4600  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07043A  
; FILING DATE: June 21, 1994  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/10889  
; FILING DATE: November 12, 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/995,660  
; FILING DATE: December 16, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/880,914  
; FILING DATE: May 11, 1992

; ATTORNEY/AGENT INFORMATION:



; NAME: Pamela A. Simonton  
 ; REGISTRATION NUMBER: 31,060  
 ; REFERENCE/DOCKET NUMBER: MTI 224.3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (203) 937-2340  
 ; TELEFAX: (203) 937-2795  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 PCT-US94-07043A-7

Query Match 100.0%; Score 8; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0005;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 3 EVKMDAEF 10

RESULT 13

PCT-US94-07043A-2

; Sequence 2, Application PC/TUS9407043A

; GENERAL INFORMATION:

; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,  
 ; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard  
 ; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC  
 ; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Miles Inc.  
 ; STREET: 400 Morgan Lane  
 ; CITY: West Haven  
 ; STATE: Connecticut  
 ; COUNTRY: USA  
 ; ZIP: 06516

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
 ; COMPUTER: Sharp PC 4600  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07043A  
 ; FILING DATE: June 21, 1994  
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/10889  
 ; FILING DATE: November 12, 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/995,660  
 ; FILING DATE: December 16, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/880,914  
 ; FILING DATE: May 11, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Pamela A. Simonton  
; REGISTRATION NUMBER: 31,060  
; REFERENCE/DOCKET NUMBER: MTI 224.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203) 937-2340  
; TELEFAX: (203) 937-2795  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US94-07043A-2

Query Match 100.0%; Score 8; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00054;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 3 EVKMDAEF 10

RESULT 14

US-09-548-372D-71

; Sequence 71, Application US/09548372D

; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280I

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 71

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: peptide

US-09-548-372D-71

Query Match 100.0%; Score 8; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00067;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

Db                   |||||  
                    4 EVKMDAEF 11

RESULT 15

US-09-548-367D-71

; Sequence 71, Application US/09548367D

; Patent No. 6440698

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280H

; CURRENT APPLICATION NUMBER: US/09/548,367D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 71

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: peptide

US-09-548-367D-71

Query Match                   100.0%;   Score 8;   DB 4;   Length 15;

Best Local Similarity   100.0%;   Pred. No. 0.00067;

Matches       8;   Conservative       0;   Mismatches       0;   Indels       0;   Gaps       0;

Qy               1 EVKMDAEF 8

|||||

Db               4 EVKMDAEF 11

RESULT 16

US-09-551-853D-71

; Sequence 71, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR  
AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

```
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-551-853D-71
```

```
Query Match          100.0%; Score 8; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          1 EVKMDAEF 8
             |||||
Db          4 EVKMDAEF 11
```

#### RESULT 17

PCT-US94-07043A-1

```
; Sequence 1, Application PC/TUS9407043A
; GENERAL INFORMATION:
; APPLICANT: Tamburini, Paul P.; Benz, G nter; H bich,
; APPLICANT: Dieter; Dreyer, Robert N.; Koenig, Gerhard
; TITLE OF INVENTION: CATHEPSIN D IS AN AMYLOIDOGENIC
; TITLE OF INVENTION: PROTEASE IN ALZHEIMER S DISEASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miles Inc.
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
; COMPUTER: Sharp PC 4600
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07043A
; FILING DATE: June 21, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10889
; FILING DATE: November 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/995,660
; FILING DATE: December 16, 1992
; PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: 07/880,914  
; FILING DATE: May 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pamela A. Simonton  
; REGISTRATION NUMBER: 31,060  
; REFERENCE/DOCKET NUMBER: MTI 224.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203) 937-2340  
; TELEFAX: (203) 937-2795  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
PCT-US94-07043A-1

Query Match 100.0%; Score 8; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.00071;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 3 EVKMDAEF 10

RESULT 18

US-08-802-981-114

; Sequence 114, Application US/08802981  
; Patent No. 6037137

; GENERAL INFORMATION:

; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly S.  
; TITLE OF INVENTION: Compositions for the Detection of Enzyme  
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use  
Thereof

; NUMBER OF SEQUENCES: 231

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/802,981  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 016865-000300US  
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Acp"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
US-08-802-981-114

```

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Query Match          100.0%; Score 8; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy          1 EVKMDAEF 8
             |||||
Db          7 EVKMDAEF 14

```

# RESULT 19

US-08-141-324-11

```

; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-141-324-11

```

```

Query Match          100.0%; Score 8; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      5 EVKMDAEF 12

```

RESULT 20

US-08-541-902-11

```

; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

```



; APPLICATION NUMBER: US/08/541,902  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/141,324  
 ; FILING DATE: 21-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ferber, Donna M.  
 ; REGISTRATION NUMBER: 33,878  
 ; REFERENCE/DOCKET NUMBER: 44-93  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 303-499-8080  
 ; TELEFAX: 303-499-8089  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 27 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-08-541-902-11

Query Match 100.0%; Score 8; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 5 EVKMDAEF 12

# RESULT 21

US-08-462-859A-5

; Sequence 5, Application US/08462859A

; Patent No. 5652092

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
 Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-5

```

```

Query Match          100.0%; Score 8; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          1 EVKMDAEF 8
            |||||
Db          6 EVKMDAEF 13

```

# RESULT 22

US-08-123-659A-5

```

; Sequence 5, Application US/08123659A
; Patent No. 5656477

```

## ; GENERAL INFORMATION:

```

; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate
Formation

```

```

; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19

```

## ; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054

```

## ; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

## ; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Rosenblum, Anne M.
;   REGISTRATION NUMBER: 30,419
;   REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (518)475-0611
;   TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 5:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 45 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-123-659A-5

```

```

Query Match          100.0%; Score 8; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      6 EVKMDAEF 13

```

RESULT 23

US-08-464-247A-5

; Sequence 5, Application US/08464247A

; Patent No. 5693478

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,247A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2158  
; TELEFAX: 201-683-4117  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-464-247A-5

Query Match 100.0%; Score 8; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 6 EVKMDAEF 13

RESULT 24

US-08-464-248A-5

; Sequence 5, Application US/08464248A

; Patent No. 5703209

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,248A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246

; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-464-248A-5

Query Match 100.0%; Score 8; DB 1; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 6 EVKMDAEF 13

RESULT 25

US-08-371-930-25

; Sequence 25, Application US/08371930  
; Patent No. 5578451

; GENERAL INFORMATION:

; APPLICANT: Nishimoto, Ikuo  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/371,930  
; FILING DATE:  
; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/019,208  
; FILING DATE: February 18, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/154001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 58  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

US-08-371-930-25

Query Match 100.0%; Score 8; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 43 EVKMDAEF 50

RESULT 26

PCT-US94-01712-25

; Sequence 25, Application PC/TUS9401712

; GENERAL INFORMATION:

; APPLICANT: Nishimoto, Ikuo

; TITLE OF INVENTION: ALZHEIMER'S DISEASE THERAPEUTICS

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/01712

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/019,208

; FILING DATE: February 18, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00786/154001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 58

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

PCT-US94-01712-25

Query Match 100.0%; Score 8; DB 5; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
|||||||  
Db 43 EVKMDAEF 50

RESULT 27

US-08-484-969-3

; Sequence 3, Application US/08484969

; Patent No. 5679531

; GENERAL INFORMATION:

; APPLICANT: Konig, Gerhard

; APPLICANT: Graham, Paul

; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4

; TITLE OF INVENTION: Peptide

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Allegretti & Witcoff, Ltd.

; STREET: 10 South Wacker Drive Suite 3000

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,969

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: McDonnell, John J

; REGISTRATION NUMBER: 26,949

; REFERENCE/DOCKET NUMBER: 95,216

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-715-1000

; TELEFAX: 312-715-1234

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 59 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Cleavage-site

; LOCATION: 4..5

; OTHER INFORMATION: /label= Beta

; OTHER INFORMATION: /note= "Beta cleavage site in APP"

; FEATURE:

; NAME/KEY: Cleavage-site

; LOCATION: 20..21

; OTHER INFORMATION: /label= Alpha

; OTHER INFORMATION: /note= "Alpha cleavage site in APP, residues 16/17

; OTHER INFORMATION: of BA4."

; FEATURE:



```

; NAME/KEY: Cleavage-site
; LOCATION: 46..47
; OTHER INFORMATION: /label= Gamma
; OTHER INFORMATION: /note= "Gamma cleavage site in APP"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 5..47
; OTHER INFORMATION: /label= BA4
; OTHER INFORMATION: /note= "BA4 peptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 33..56
; OTHER INFORMATION: /label= Tm
; OTHER INFORMATION: /note= "Transmembrane region of APP"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..32
; OTHER INFORMATION: /label= Ex
; OTHER INFORMATION: /note= "N-terminal extracellular part of APP"
US-08-484-969-3

```

```

Query Match          100.0%; Score 8; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      1 EVKMDAEF 8

```

RESULT 28

US-08-472-627-3

```

; Sequence 3, Application US/08472627
; Patent No. 5693753
; GENERAL INFORMATION:
; APPLICANT: Konig, Gerhard
; APPLICANT: Graham, Paul
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4
; TITLE OF INVENTION: Peptide
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,627
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: McDonnell, John J
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 95,216
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 4..5
; OTHER INFORMATION: /label= Beta
; OTHER INFORMATION: /note= "Beta cleavage site in APP"
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 20..21
; OTHER INFORMATION: /label= Alpha
; OTHER INFORMATION: /note= "Alpha cleavage site in APP, residues 16/17
; OTHER INFORMATION: of BA4."
; FEATURE:
; NAME/KEY: Cleavage-site
; LOCATION: 46..47
; OTHER INFORMATION: /label= Gamma
; OTHER INFORMATION: /note= "Gamma cleavage site in APP"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 5..47
; OTHER INFORMATION: /label= BA4
; OTHER INFORMATION: /note= "BA4 peptide"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 33..56
; OTHER INFORMATION: /label= Tm
; OTHER INFORMATION: /note= "Transmembrane region of APP"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..32
; OTHER INFORMATION: /label= Ex
; OTHER INFORMATION: /note= "N-terminal extracellular part of APP"
US-08-472-627-3

```

```

Query Match          100.0%; Score 8; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      1 EVKMDAEF 8

```

```

RESULT 29
US-08-388-463-3

```

; Sequence 3, Application US/08388463  
; Patent No. 5786180  
; GENERAL INFORMATION:  
; APPLICANT: Konig, Gerhard  
; APPLICANT: Graham, Paul  
; TITLE OF INVENTION: Monoclonal Antibody Specific for BA4  
; TITLE OF INVENTION: Peptide  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Allegretti & Witcoff, Ltd.  
; STREET: 10 South Wacker Drive Suite 3000  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 95,216  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 59 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 4..5  
; OTHER INFORMATION: /label= Beta  
; OTHER INFORMATION: /note= "Beta cleavage site in APP"  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 20..21  
; OTHER INFORMATION: /label= Alpha  
; OTHER INFORMATION: /note= "Alpha cleavage site in APP, residues 16/17  
; OTHER INFORMATION: of BA4."  
; FEATURE:  
; NAME/KEY: Cleavage-site  
; LOCATION: 46..47  
; OTHER INFORMATION: /label= Gamma  
; OTHER INFORMATION: /note= "Gamma cleavage site in APP"  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 5..47

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;   OTHER INFORMATION:  /label= BA4
;   OTHER INFORMATION:  /note= "BA4 peptide"
;   FEATURE:
;   NAME/KEY:  Region
;   LOCATION:  33..56
;   OTHER INFORMATION:  /label= Tm
;   OTHER INFORMATION:  /note= "Transmembrane region of APP"
;   FEATURE:
;   NAME/KEY:  Region
;   LOCATION:  1..32
;   OTHER INFORMATION:  /label= Ex
;   OTHER INFORMATION:  /note= "N-terminal extracellular part of APP"
US-08-388-463-3

```

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Query Match          100.0%;  Score 8;  DB 1;  Length 59;
Best Local Similarity 100.0%;  Pred. No. 0.0024;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          1 EVKMDAEF 8
            |||||
Db          1 EVKMDAEF 8

```

RESULT 30

US-08-462-859A-3

; Sequence 3, Application US/08462859A

; Patent No. 5652092

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Cyanamid Plaza

; CITY: Wayne

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,859A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246

; TELEFAX: (201)831-3305  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-462-859A-3

Query Match 100.0%; Score 8; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 6 EVKMDAEF 13

RESULT 31

US-08-462-859A-4

; Sequence 4, Application US/08462859A  
; Patent No. 5652092

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.  
; APPLICANT: Vitek, M. P.  
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of  
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 07470-8426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,859A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 31,844-04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201)831-3246  
; TELEFAX: (201)831-3305

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids

; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-462-859A-4

Query Match 100.0%; Score 8; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
| | | | | | | |  
Db 6 EVKMDAEF 13

RESULT 32

US-08-123-659A-3

; Sequence 3, Application US/08123659A  
; Patent No. 5656477

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Anne Rosenblum

; STREET: 163 Delaware Avenue, Suite 212

; CITY: Delmar

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 12054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123,659A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Rosenblum, Anne M.

; REGISTRATION NUMBER: 30,419

; REFERENCE/DOCKET NUMBER: 31,844-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (518)475-0611

; TELEFAX: (518)475-0619

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-659A-3

Query Match 100.0%; Score 8; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
      |||||||  
Db 6 EVKMDAEF 13

RESULT 33

US-08-123-659A-4

; Sequence 4, Application US/08123659A

; Patent No. 5656477

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Anne Rosenblum

; STREET: 163 Delaware Avenue, Suite 212

; CITY: Delmar

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 12054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/123,659A

; FILING DATE: 20-SEP-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Rosenblum, Anne M.

; REGISTRATION NUMBER: 30,419

; REFERENCE/DOCKET NUMBER: 31,844-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (518)475-0611

; TELEFAX: (518)475-0619

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-123-659A-4

Query Match 100.0%; Score 8; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 EVKMDAEF 8  
|||||||  
Db 6 EVKMDAEF 13

RESULT 34

US-08-464-247A-3

; Sequence 3, Application US/08464247A

; Patent No. 5693478

; GENERAL INFORMATION:

; APPLICANT: Jacobsen, J. S.

; APPLICANT: Vitek, M. P.

; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of

; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
Formation

; TITLE OF INVENTION: of B-Amyloid Peptide

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: One Campus Drive

; CITY: Parsippany

; STATE: New Jersey

; COUNTRY: United States

; ZIP: 07054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,247A

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Barnhard, Elizabeth M.

; REGISTRATION NUMBER: 31,088

; REFERENCE/DOCKET NUMBER: 31,844-03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-683-2158

; TELEFAX: 201-683-4117

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 63 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-464-247A-3

Query Match 100.0%; Score 8; DB 1; Length 63;

Best Local Similarity 100.0%; Pred. No. 0.0025;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 6 EVKMDAEF 13

RESULT 35

US-08-464-247A-4

```
; Sequence 4, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
;   APPLICANT:  Jacobsen, J. S.
;   APPLICANT:  Vitek, M. P.
;   TITLE OF INVENTION:  No. 5693478el Amyloid Precursor and Method of
;   TITLE OF INVENTION:  Using Same to Access Agents Which Down-Regulate
Formation
;   TITLE OF INVENTION:  of B-Amyloid Peptide
;   NUMBER OF SEQUENCES:  19
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  American Cyanamid Company
;     STREET:    One Campus Drive
;     CITY:      Parsippany
;     STATE:     New Jersey
;     COUNTRY:   United States
;     ZIP:       07054
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:    IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:    PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/464,247A
;     FILING DATE:       05-JUN-1995
;     CLASSIFICATION:    435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Barnhard, Elizabeth M.
;     REGISTRATION NUMBER:  31,088
;     REFERENCE/DOCKET NUMBER:  31,844-03
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  201-683-2158
;     TELEFAX:   201-683-4117
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  63 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
```

US-08-464-247A-4

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Query Match          100.0%;  Score 8;  DB 1;  Length 63;
Best Local Similarity 100.0%;  Pred. No. 0.0025;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;
```

```
Qy          1 EVKMDAEF 8
             |||||
Db          6 EVKMDAEF 13
```

RESULT 36

US-08-464-248A-3

```
; Sequence 3, Application US/08464248A
```

```

; Patent No. 5703209
; GENERAL INFORMATION:
;   APPLICANT:  Jacobsen, J. S.
;   APPLICANT:  Vitek, M. P.
;   TITLE OF INVENTION:  No. 5703209e1 Amyloid Precursor and Method of
;   TITLE OF INVENTION:  Using Same to Access Agents Which Down-Regulate
Formation
;   TITLE OF INVENTION:  of B-Amyloid Peptide
;   NUMBER OF SEQUENCES:  19
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  American Cyanamid Company
;     STREET:    One Cyanamid Plaza
;     CITY:      Wayne
;     STATE:     New Jersey
;     COUNTRY:   United States
;     ZIP:       07470-8426
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:    IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:    PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/464,248A
;     FILING DATE:       05-JUN-1995
;     CLASSIFICATION:    435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Barnhard, Elizabeth M.
;     REGISTRATION NUMBER:  31,088
;     REFERENCE/DOCKET NUMBER:  31,844-02
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (201)831-3246
;     TELEFAX:   (201)831-3305
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  63 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-464-248A-3

```

```

Query Match          100.0%;  Score 8;  DB 1;  Length 63;
Best Local Similarity 100.0%;  Pred. No. 0.0025;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          1 EVKMDAEF 8
             |||||
Db          6 EVKMDAEF 13

```

RESULT 37

```

US-08-464-248A-4
; Sequence 4, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
;   APPLICANT:  Jacobsen, J. S.
;   APPLICANT:  Vitek, M. P.

```

; TITLE OF INVENTION: No. 5703209e1 Amyloid Precursor and Method of  
 ; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate  
 Formation  
 ; TITLE OF INVENTION: of B-Amyloid Peptide  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: American Cyanamid Company  
 ; STREET: One Cyanamid Plaza  
 ; CITY: Wayne  
 ; STATE: New Jersey  
 ; COUNTRY: United States  
 ; ZIP: 07470-8426  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/464,248A  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barnhard, Elizabeth M.  
 ; REGISTRATION NUMBER: 31,088  
 ; REFERENCE/DOCKET NUMBER: 31,844-02  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201)831-3246  
 ; TELEFAX: (201)831-3305  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 63 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-464-248A-4

Query Match 100.0%; Score 8; DB 1; Length 63;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 6 EVKMDAEF 13

RESULT 38

US-09-027-258-1

; Sequence 1, Application US/09027258

; Patent No. 6670182

; GENERAL INFORMATION:

; APPLICANT: Pruss, Rebecca  
 ; APPLICANT: Huggins, John  
 ; APPLICANT: Rautmann, Guy  
 ; APPLICANT: Cordell, Barbara  
 ; APPLICANT: Scardina, Jan  
 ; APPLICANT: Mischak, Ron

```

; TITLE OF INVENTION: IMPROVED ASSAYS FOR BETA-AMYLOID
; TITLE OF INVENTION: PROCESSING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,258
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marsh, David R
; REGISTRATION NUMBER: P-41,182
; REFERENCE/DOCKET NUMBER: 03561.0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6904
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6670182e
US-09-027-258-1

```

```

Query Match          100.0%; Score 8; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          1 EVKMDAEF 8
             |||||
Db          22 EVKMDAEF 29

```

RESULT 39

US-08-404-831-2

```

; Sequence 2, Application US/08404831
; Patent No. 5817626

```

; GENERAL INFORMATION:

```

; APPLICANT: Mark A. Findeis, Howard Benjamin, Marc B. Garnick,
; APPLICANT: Malcolm L. Gefter, Arvind Hundal, Laura Kasman,
; APPLICANT: Gary Musso, Ethan R. Signer, and James Wakefield

```

; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide  
 Aggrega  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 State Street, Suite 510  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/404,831  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hanley, Elizabeth A. (EAH)  
 ; REGISTRATION NUMBER: 33,505  
 ; REFERENCE/DOCKET NUMBER: PPI-002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617)227-7400  
 ; TELEFAX: (617)227-5941  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 103 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 US-08-404-831-2

Query Match 100.0%; Score 8; DB 2; Length 103;  
 Best Local Similarity 100.0%; Pred. No. 0.004;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
 |||||  
 Db 1 EVKMDAEF 8

# RESULT 40

US-08-612-785B-2

; Sequence 2, Application US/08612785B

; Patent No. 5854204

; GENERAL INFORMATION:

; APPLICANT: Findeis, Mark A. et al.

; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid

; TITLE OF INVENTION: Aggregation

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-2

```

```

Query Match          100.0%; Score 8; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      1 EVKMDAEF 8

```

```

Search completed: March 26, 2004, 15:36:08
Job time : 32.5 secs

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OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:37 ; Search time 13.5 Seconds  
(without alignments)  
57.002 Million cell updates/sec

Title: US-09-668-314C-70  
Perfect score: 8  
Sequence: 1 EVKMDAEF 8

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR\_78:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	%	Length	DB	ID	Description
1	8	100.0	33	2	S23094	beta-amyloid prote	
2	8	100.0	57	2	E60045	Alzheimer's diseas	
3	8	100.0	57	2	F60045	Alzheimer's diseas	
4	8	100.0	57	2	G60045	Alzheimer's diseas	
5	8	100.0	57	2	D60045	Alzheimer's diseas	
6	8	100.0	57	2	A60045	Alzheimer's diseas	
7	8	100.0	57	2	B60045	Alzheimer's diseas	
8	8	100.0	82	2	PQ0438	Alzheimer's diseas	
9	8	100.0	695	1	A49795	Alzheimer's diseas	
10	8	100.0	695	2	A27485	Alzheimer's diseas	
11	8	100.0	695	2	S00550	Alzheimer's diseas	
12	8	100.0	770	1	QRHUA4	Alzheimer's diseas	
13	5	62.5	84	2	T27174	hypothetical prote	

14	5	62.5	105	2	PH1526	gamma-aminobutyric
15	5	62.5	127	2	H90315	conserved hypothet
16	5	62.5	140	2	T21857	hypothetical prote
17	5	62.5	146	2	C69136	hypothetical prote
18	5	62.5	153	2	A95928	probable amine oxi
19	5	62.5	168	2	S73644	hypothetical prote
20	5	62.5	179	2	C95230	hypothetical prote
21	5	62.5	179	2	F98094	conserved hypothet
22	5	62.5	196	2	S73668	hypothetical prote
23	5	62.5	205	2	T11657	rho GDP dissociati
24	5	62.5	218	2	T30415	host range factor
25	5	62.5	220	2	I55963	Lyt-2.1 lymphocyte
26	5	62.5	224	2	S59147	cytochrome-c oxida
27	5	62.5	229	2	E34284	cytochrome-c oxida
28	5	62.5	229	2	T11796	cytochrome-c oxida
29	5	62.5	230	2	D58892	cytochrome-c oxida
30	5	62.5	230	2	S36009	cytochrome-c oxida
31	5	62.5	230	2	S45491	cytochrome-c oxida
32	5	62.5	230	2	T09860	cytochrome-c oxida
33	5	62.5	230	2	T09950	cytochrome-c oxida
34	5	62.5	230	2	T11290	cytochrome-c oxida
35	5	62.5	230	2	T11303	cytochrome-c oxida
36	5	62.5	230	2	T11537	cytochrome-c oxida
37	5	62.5	230	2	T11767	cytochrome-c oxida
38	5	62.5	232	2	E84673	hypothetical prote
39	5	62.5	234	2	S35465	cytochrome-c oxida
40	5	62.5	246	2	A29523	T-cell surface gly
41	5	62.5	247	1	RWMST2	T-cell surface gly
42	5	62.5	247	2	A34954	T-cell surface gly
43	5	62.5	248	2	T11893	cytochrome-c oxida
44	5	62.5	276	2	S39702	transcription anti
45	5	62.5	284	2	A40590	lateral flagellin
46	5	62.5	288	2	T48268	DP-2 transcription
47	5	62.5	320	2	AD3435	cytochrome-c oxida
48	5	62.5	363	2	S55035	peroxidase (EC 1.1
49	5	62.5	366	2	D81521	conserved hypothet
50	5	62.5	369	2	E86554	Fe-S oxidoreductas
51	5	62.5	369	2	G72069	conserved hypothet
52	5	62.5	370	2	T48633	hypothetical prote
53	5	62.5	371	2	D75266	cell division prot
54	5	62.5	371	2	S30978	integrase - Mycoba
55	5	62.5	375	2	G72018	chlps 43 kda prote
56	5	62.5	375	2	F86606	CHLPS 43 kDa prote
57	5	62.5	396	2	AH1426	peptidases homolog
58	5	62.5	408	2	F70369	carboxyl-terminal
59	5	62.5	419	1	H69349	diaminopimelate de
60	5	62.5	427	2	F85436	hypothetical prote
61	5	62.5	430	2	T37549	hypothetical prote
62	5	62.5	452	2	S56938	fructose-2,6-bisph
63	5	62.5	453	2	H70352	mannose-6-phosphat
64	5	62.5	457	2	A27449	T-cell surface gly
65	5	62.5	461	2	T43679	A/G-specific adeni
66	5	62.5	461	2	T38390	A/G-specific adeni
67	5	62.5	464	2	T38356	septin homolog spn
68	5	62.5	476	2	A39406	dihydrolipoamide d
69	5	62.5	478	2	T05102	hypothetical prote
70	5	62.5	489	2	S68280	protein disulfide-

71	5	62.5	494	2	AD3255	l-sorbose dehydrog
72	5	62.5	534	1	P1WL41	L1 protein - human
73	5	62.5	615	2	T29550	hypothetical prote
74	5	62.5	627	2	S48968	NDT80 protein - ye
75	5	62.5	633	2	B83478	probable two-compo
76	5	62.5	715	2	AB2210	anthranilate synth
77	5	62.5	743	2	D84854	hypothetical prote
78	5	62.5	747	2	JH0773	Alzheimer's diseas
79	5	62.5	855	2	S77252	phosphorylase (EC
80	5	62.5	905	2	T40015	phosphatidylethano
81	5	62.5	927	2	T38127	phosphoprotein - f
82	5	62.5	929	2	T52517	hypothetical prote
83	5	62.5	938	2	T01809	hypothetical prote
84	5	62.5	947	2	B86231	hypothetical prote
85	5	62.5	996	2	T18717	hypothetical prote
86	5	62.5	1007	2	H72734	hypothetical prote
87	5	62.5	1290	2	JC5473	dextranucrase (EC
88	5	62.5	1334	2	T19493	hypothetical prote
89	5	62.5	1564	2	T27121	hypothetical prote
90	5	62.5	2245	2	T18278	myosin heavy chain
91	5	62.5	2960	2	A45259	desmoyokin - human
92	5	62.5	3351	2	T13812	lipophorin - fruit
93	5	62.5	4450	2	JX0340	gramicidin S synth
94	5	62.5	4452	1	YGBSG2	gramicidin S synth
95	4	50.0	25	2	S68005	hucolin, 35K chain
96	4	50.0	29	2	A27561	Meth A tumor-speci
97	4	50.0	30	2	S69269	ezrin homolog - bo
98	4	50.0	34	2	A84391	hypothetical prote
99	4	50.0	42	2	PN0512	beta-amyloid prote
100	4	50.0	52	1	RUME	rubredoxin - Megas
101	4	50.0	61	2	H82090	hypothetical prote
102	4	50.0	66	2	S10561	chlorophyll a/b-bi
103	4	50.0	67	2	T40218	probable ATP synth
104	4	50.0	68	2	JH0113	protein-tyrosine k
105	4	50.0	69	2	D72403	hypothetical prote
106	4	50.0	71	2	B81812	hypothetical prote
107	4	50.0	72	2	E69386	hypothetical prote
108	4	50.0	73	2	S40015	phd protein - phag
109	4	50.0	73	2	F82784	hypothetical prote
110	4	50.0	74	2	AH1317	ferredoxin homolog
111	4	50.0	74	2	AH1689	ferredoxin homolog
112	4	50.0	74	2	F96670	hypothetical prote
113	4	50.0	74	2	H84256	hypothetical prote
114	4	50.0	75	2	S01148	H+-transporting tw
115	4	50.0	75	2	C82684	conserved hypothet
116	4	50.0	75	2	H96954	feoA protein, invo
117	4	50.0	75	2	A97799	hypothetical prote
118	4	50.0	77	2	F69219	conserved hypothet
119	4	50.0	77	2	C72808	gp68 protein - Myc
120	4	50.0	78	2	H84353	hypothetical prote
121	4	50.0	82	2	AB0272	hypothetical prote
122	4	50.0	84	2	S43801	hypothetical prote
123	4	50.0	85	2	T47563	kinetochore-like p
124	4	50.0	86	2	AI2955	cell division topo
125	4	50.0	86	2	D98327	cell division topo
126	4	50.0	87	2	T29724	hypothetical prote
127	4	50.0	90	2	C81917	hypothetical prote

128	4	50.0	90	2	A81186	hypothetical prote
129	4	50.0	90	2	AD3625	cell division inhi
130	4	50.0	92	2	C69554	conserved hypothet
131	4	50.0	92	2	T12859	hypothetical prote
132	4	50.0	93	2	T23016	hypothetical prote
133	4	50.0	94	2	JN0660	heat shock protein
134	4	50.0	94	2	S68248	chaperonin groES -
135	4	50.0	94	2	S32105	chaperonin groES -
136	4	50.0	94	2	S23685	erythrocyte membra
137	4	50.0	96	2	T46826	muconolactone Delt
138	4	50.0	97	2	T34056	hypothetical prote
139	4	50.0	98	2	A37397	hypothetical prote
140	4	50.0	99	2	B46598	ski-related protei
141	4	50.0	99	2	A97821	10K chaperonin [im
142	4	50.0	100	2	AI2298	cobalt transport p
143	4	50.0	103	2	AC1582	thioredoxin [impor
144	4	50.0	103	2	AI1228	thioredoxin [impor
145	4	50.0	103	2	T03013	hypothetical prote
146	4	50.0	104	2	H95206	thioredoxin [impor
147	4	50.0	104	2	H98071	thioredoxin-disulf
148	4	50.0	104	2	C70300	ribosomal protein
149	4	50.0	105	2	T37632	hypothetical prote
150	4	50.0	105	2	AD2301	hypothetical prote
151	4	50.0	107	2	C41043	hypothetical prote
152	4	50.0	109	2	S77444	hypothetical prote
153	4	50.0	109	2	B64145	hypothetical prote
154	4	50.0	111	1	A32233	thioredoxin 2 [val
155	4	50.0	114	2	D64345	hypothetical prote
156	4	50.0	115	2	AF2098	thioredoxin 2 [imp
157	4	50.0	115	2	E84340	hypothetical prote
158	4	50.0	115	2	E97483	hypothetical prote
159	4	50.0	116	2	T49862	related to REM1 pr
160	4	50.0	118	2	AB1604	B. subtilis YqzD p
161	4	50.0	119	2	A64887	ydaY protein - Esc
162	4	50.0	119	2	T17032	fimbriata-associat
163	4	50.0	119	2	AE1580	hypothetical prote
164	4	50.0	121	2	A69110	hypothetical prote
165	4	50.0	123	2	S55326	pseudoazurin - Thi
166	4	50.0	124	2	B87345	hypothetical prote
167	4	50.0	125	2	H86722	hypothetical prote
168	4	50.0	125	2	A83048	hypothetical prote
169	4	50.0	125	2	AF2032	hypothetical prote
170	4	50.0	128	2	C82474	MutT/nudix family
171	4	50.0	129	2	S48814	hypothetical prote
172	4	50.0	130	2	H84200	hypothetical prote
173	4	50.0	130	2	T20762	hypothetical prote
174	4	50.0	131	2	AF0510	transcription acti
175	4	50.0	133	2	G89889	cell division prot
176	4	50.0	134	2	AD3503	bacterial protein
177	4	50.0	134	2	S61844	ferric uptake tran
178	4	50.0	134	2	A40622	ferric uptake regu
179	4	50.0	134	2	G69444	hypothetical prote
180	4	50.0	135	2	B82794	conserved hypothet
181	4	50.0	136	1	D69495	conserved hypothet
182	4	50.0	138	2	AG2808	diacylglycerol kin
183	4	50.0	138	2	E97587	diacylglycerol kin
184	4	50.0	138	2	G71002	probable glycine c

185	4	50.0	138	2	T47152	hypothetical prote
186	4	50.0	140	2	B36945	flagellar biosynth
187	4	50.0	140	2	AD0639	flagella synthesis
188	4	50.0	140	2	A69445	hypothetical prote
189	4	50.0	141	2	AC1556	regulatory protein
190	4	50.0	141	2	AE1198	regulatory protein
191	4	50.0	142	2	A87501	hypothetical prote
192	4	50.0	142	2	E89026	protein F13A2.1 [i
193	4	50.0	142	2	E84069	hypothetical prote
194	4	50.0	143	2	B86853	hypothetical prote
195	4	50.0	143	2	E89419	protein AC8.6 [imp
196	4	50.0	143	2	T18599	hypothetical prote
197	4	50.0	144	2	E75128	glycine cleavage s
198	4	50.0	144	2	B95242	hypothetical prote
199	4	50.0	144	2	E98106	conserved hypothet
200	4	50.0	145	2	T02016	DNA-binding protei
201	4	50.0	145	2	S62510	hypothetical prote
202	4	50.0	145	2	F75189	hypothetical prote
203	4	50.0	147	2	S75581	hypothetical prote
204	4	50.0	147	2	T19162	hypothetical prote
205	4	50.0	148	2	AH1166	ribose 5-phosphate
206	4	50.0	149	2	F86380	protein F5A9.10 [i
207	4	50.0	149	2	T51471	farnesylated prote
208	4	50.0	149	2	AB1395	hypothetical prote
209	4	50.0	149	2	AE1770	hypothetical prote
210	4	50.0	150	2	AB2857	pseudoazurin [impo
211	4	50.0	150	2	S22328	gene D protein - p
212	4	50.0	150	2	G84585	probable kinetecho
213	4	50.0	150	2	AI1968	hypothetical prote
214	4	50.0	150	2	S10913	hypothetical prote
215	4	50.0	151	2	AC0407	ribose-5-phosphate
216	4	50.0	151	2	A69539	maoC protein (maoC
217	4	50.0	152	2	T04479	cinnamyl-alcohol d
218	4	50.0	152	2	AF2680	transcription regu
219	4	50.0	152	2	D97462	hypothetical prote
220	4	50.0	152	2	H96734	probable isoprenyl
221	4	50.0	152	2	T48054	hypothetical prote
222	4	50.0	153	2	B84697	probable small hea
223	4	50.0	153	2	PN0564	von Willebrand fac
224	4	50.0	153	2	D90594	hypothetical prote
225	4	50.0	153	2	T05686	farnesylated prote
226	4	50.0	154	2	B81810	hypothetical prote
227	4	50.0	154	2	D71455	hypothetical prote
228	4	50.0	154	2	T47825	Skp1-like protein
229	4	50.0	154	2	AC0242	probable exported
230	4	50.0	155	2	G96622	probable Heat shoc
231	4	50.0	155	2	H81363	probable RNA methy
232	4	50.0	155	2	F75040	hypothetical prote
233	4	50.0	156	2	E69808	protein-tyrosine p
234	4	50.0	156	2	B64036	hypothetical prote
235	4	50.0	159	2	AC2533	hypothetical prote
236	4	50.0	159	2	C69390	conserved hypothet
237	4	50.0	160	2	AI1308	dihydrofolate redu
238	4	50.0	160	2	AI1680	dihydrofolate redu
239	4	50.0	160	2	D69096	formate hydrogenly
240	4	50.0	160	2	B39128	hypothetical prote
241	4	50.0	160	2	B70302	hypothetical prote

242	4	50.0	161	2	B70323	lipopolysaccharide
243	4	50.0	161	2	T48285	hypothetical prote
244	4	50.0	162	2	F71413	probable S-linaloo
245	4	50.0	162	2	S17803	hypothetical prote
246	4	50.0	164	2	H65086	hypothetical prote
247	4	50.0	164	2	F91114	hypothetical prote
248	4	50.0	164	2	F85959	hypothetical prote
249	4	50.0	164	2	AI0885	probable membrane
250	4	50.0	166	2	B64724	transcription acti
251	4	50.0	166	2	E90633	transcription regu
252	4	50.0	166	2	E85484	transcription regu
253	4	50.0	166	2	T08580	hypothetical prote
254	4	50.0	167	1	RDSODF	dihydrofolate redu
255	4	50.0	167	2	T22198	hypothetical prote
256	4	50.0	168	2	T14723	antirestriction pr
257	4	50.0	170	1	HMECBM	M-agglutinin precu
258	4	50.0	170	2	T02707	probable kinetecho
259	4	50.0	170	2	T08348	hypothetical prote
260	4	50.0	172	2	S32489	lectin - Iberian r
261	4	50.0	172	2	T10346	hypothetical prote
262	4	50.0	172	2	E81296	probable periplasm
263	4	50.0	172	2	H81251	NADH2 dehydrogenas
264	4	50.0	173	2	G64318	hypothetical prote
265	4	50.0	173	2	B75178	mutator protein mu
266	4	50.0	173	2	C64115	riboflavin synthas
267	4	50.0	173	2	B38435	regulatory protein
268	4	50.0	174	2	A48198	voltage-dependent
269	4	50.0	174	2	S27343	hupJ protein - Rhi
270	4	50.0	174	2	AI0618	conserved hypothet
271	4	50.0	175	2	D75467	bacterioferritin c
272	4	50.0	176	2	I40599	5-Nitroimidazole a
273	4	50.0	176	2	JK0226	arachin 21K chain
274	4	50.0	177	1	S74739	translation initia
275	4	50.0	177	2	T31086	probable dTDP-4-de
276	4	50.0	177	2	F95912	hypothetical prote
277	4	50.0	178	1	E69389	hypothetical prote
278	4	50.0	178	2	S26044	sex-determining pr
279	4	50.0	179	2	S62019	hypothetical prote
280	4	50.0	179	2	T22301	hypothetical prote
281	4	50.0	180	2	T44944	hypothetical prote
282	4	50.0	180	2	S76762	hypothetical prote
283	4	50.0	181	2	S73534	hypothetical prote
284	4	50.0	182	1	S73152	translation initia
285	4	50.0	182	2	E64678	NADH2 dehydrogenas
286	4	50.0	182	2	C71839	NADH2 dehydrogenas
287	4	50.0	182	2	A96666	protein F22C12.8 [
288	4	50.0	182	2	B90060	hypothetical prote
289	4	50.0	183	2	F83858	hypothetical prote
290	4	50.0	183	2	E85182	hypothetical prote
291	4	50.0	184	2	T08198	probable disease r
292	4	50.0	184	2	S26046	sex-determining pr
293	4	50.0	185	1	B69374	conserved hypothet
294	4	50.0	185	2	C86705	hypothetical prote
295	4	50.0	186	2	B87755	protein T21E12.5 [
296	4	50.0	186	2	B90548	50S ribosomal prot
297	4	50.0	186	2	T31347	hypothetical prote
298	4	50.0	187	2	T05601	probable disease r

299	4	50.0	187	2	H75489	hypothetical prote
300	4	50.0	187	2	T21671	hypothetical prote
301	4	50.0	188	2	F64336	dTMP kinase (EC 2.
302	4	50.0	188	2	T23353	hypothetical prote
303	4	50.0	189	2	T19778	hypothetical prote
304	4	50.0	189	2	D75339	hypothetical prote
305	4	50.0	189	2	T49738	hypothetical prote
306	4	50.0	189	2	H97633	pseudoazurin precu
307	4	50.0	190	2	T32265	hypothetical prote
308	4	50.0	191	2	T19804	hypothetical prote
309	4	50.0	191	2	T19803	hypothetical prote
310	4	50.0	191	2	T31594	hypothetical prote
311	4	50.0	192	2	T13225	hypothetical prote
312	4	50.0	192	2	F72338	conserved hypothet
313	4	50.0	192	2	F81372	hypothetical prote
314	4	50.0	193	2	A49704	transcription init
315	4	50.0	194	2	A83818	heat-shock protein
316	4	50.0	194	2	G82091	RNA polymerase sig
317	4	50.0	195	2	T49012	calmodulin-like pr
318	4	50.0	195	2	B70577	hypothetical prote
319	4	50.0	195	2	D87256	nitroreductase fam
320	4	50.0	195	2	D95946	probable guanylate
321	4	50.0	196	2	S01056	early light-induce
322	4	50.0	196	2	S72861	hypothetical prote
323	4	50.0	196	2	E91064	chaperone-like pro
324	4	50.0	196	2	A99857	bfpT-regulated cha
325	4	50.0	196	2	A85909	probable chaperone
326	4	50.0	196	2	B85763	probable chaperone
327	4	50.0	196	2	AI2085	two-component resp
328	4	50.0	197	2	A29648	female-specific tr
329	4	50.0	197	2	C71005	hypothetical prote
330	4	50.0	197	2	E64102	skp protein - Haem
331	4	50.0	198	2	S60215	epoxidase fom4 - S
332	4	50.0	199	2	C71979	urease accessory p
333	4	50.0	199	2	D64528	urease accessory p
334	4	50.0	199	2	H70709	hypothetical prote
335	4	50.0	199	2	AD3401	exopolysaccharide
336	4	50.0	199	2	T27428	hypothetical prote
337	4	50.0	200	2	AG0986	hypothetical luxR-
338	4	50.0	200	2	E96525	protein T1N15.21 [
339	4	50.0	201	2	D71824	hypothetical prote
340	4	50.0	202	2	H69495	conserved hypothet
341	4	50.0	202	2	T12993	hypothetical prote
342	4	50.0	202	2	A97342	nudix (MutT) famil
343	4	50.0	203	1	S45869	glutaredoxin homol
344	4	50.0	204	2	AG2383	translation initia
345	4	50.0	204	2	G83034	urease accessory p
346	4	50.0	204	2	T44495	hypothetical prote
347	4	50.0	205	2	G75535	deoxyguanosine kin
348	4	50.0	205	2	T08049	proliferating cell
349	4	50.0	206	2	S50913	TAF25 protein - ye
350	4	50.0	206	2	A97943	hypothetical prote
351	4	50.0	207	2	F98283	hypothetical prote
352	4	50.0	208	2	AC2830	pyrazinamidase/nic
353	4	50.0	208	2	F95892	probable glutathio
354	4	50.0	209	2	C35385	hydrogen dehydroge
355	4	50.0	209	2	T19847	hypothetical prote



356	4	50.0	209	2	T35041	hypothetical prote
357	4	50.0	210	2	G95858	probable 3-octapre
358	4	50.0	210	2	B42938	F-pilus assembly p
359	4	50.0	210	2	F75126	hypothetical prote
360	4	50.0	211	2	E70253	hypothetical prote
361	4	50.0	212	2	E75334	ribonuclease HII -
362	4	50.0	212	2	I50543	aryl hydrocarbon r
363	4	50.0	213	2	F87669	conserved hypothet
364	4	50.0	214	2	D96839	F23A5.5 [imported]
365	4	50.0	214	2	H96842	F23A5.34 [imported]
366	4	50.0	214	2	A87276	hypothetical prote
367	4	50.0	215	2	AI1663	amino acid (glutam
368	4	50.0	215	2	B72640	hypothetical prote
369	4	50.0	215	2	AC1292	amino acid (glutam
370	4	50.0	216	2	E75425	hypothetical prote
371	4	50.0	216	2	AF2026	hypothetical prote
372	4	50.0	216	2	H86380	protein F5A9.6 [im
373	4	50.0	216	2	H95131	hypothetical prote
374	4	50.0	217	1	I67685	nitroreductase (EC
375	4	50.0	217	1	S08397	nitroreductase (EC
376	4	50.0	217	2	H90705	oxygen-insensitive
377	4	50.0	217	2	C85556	oxygen-insensitive
378	4	50.0	217	2	AD0573	oxygen-insensitive
379	4	50.0	217	2	T11382	cytochrome-c oxida
380	4	50.0	217	2	S65830	alpha fucosidase p
381	4	50.0	217	2	S49578	trypsin inhibitor
382	4	50.0	217	2	C83664	RNA polymerase sig
383	4	50.0	218	2	T16301	hypothetical prote
384	4	50.0	218	2	AF1190	transcription regu
385	4	50.0	218	2	AF1548	transcription regu
386	4	50.0	219	2	T47881	hypothetical prote
387	4	50.0	219	2	G95372	hypothetical prote
388	4	50.0	220	2	T34209	hypothetical prote
389	4	50.0	221	2	S30473	HIV-1 retropepsin
390	4	50.0	221	2	S77396	hypothetical prote
391	4	50.0	221	2	AI0089	probable flagellar
392	4	50.0	222	2	S10728	calcium channel pr
393	4	50.0	222	2	A46658	calcium channel pr
394	4	50.0	222	2	S51595	mycinamicin III O-
395	4	50.0	223	2	G82427	hypothetical prote
396	4	50.0	223	2	H90006	hypothetical prote
397	4	50.0	224	2	AG0406	conserved hypothet
398	4	50.0	224	2	AI3595	frnE protein [impo
399	4	50.0	225	2	T11155	cytochrome-c oxida
400	4	50.0	225	2	T11262	cytochrome-c oxida
401	4	50.0	225	2	H97607	hypothetical prote
402	4	50.0	225	2	E64075	urease accessory p
403	4	50.0	225	2	AD2429	hypothetical prote
404	4	50.0	226	1	JX0176	glutathione peroxi
405	4	50.0	226	1	A55086	glutathione peroxi
406	4	50.0	226	1	JQ0476	glutathione peroxi
407	4	50.0	226	1	JX0280	glutathione peroxi
408	4	50.0	226	2	D82454	probable glutathio
409	4	50.0	227	2	G71924	hypothetical prote
410	4	50.0	227	2	D69296	conserved hypothet
411	4	50.0	228	2	S60639	cytochrome-c oxida
412	4	50.0	228	2	T11130	cytochrome-c oxida

413	4	50.0	228	2	AC1389	B. subtilis two-co
414	4	50.0	228	2	AE1764	B. subtilis two-co
415	4	50.0	228	2	E84389	hypothetical prote
416	4	50.0	228	2	A96918	probable enzyme wi
417	4	50.0	229	2	S01503	cytochrome-c oxida
418	4	50.0	229	2	S14207	cytochrome-c oxida
419	4	50.0	229	2	S70599	cytochrome-c oxida
420	4	50.0	229	2	T11119	cytochrome-c oxida
421	4	50.0	229	2	T11277	cytochrome-c oxida
422	4	50.0	230	1	MNIV16	nonstructural prot
423	4	50.0	230	1	MNIVA5	nonstructural prot
424	4	50.0	230	1	MNIVA6	nonstructural prot
425	4	50.0	230	1	MNIVA7	nonstructural prot
426	4	50.0	230	1	MNIVA8	nonstructural prot
427	4	50.0	230	2	S68131	cytochrome-c oxida
428	4	50.0	230	2	T11457	cytochrome-c oxida
429	4	50.0	231	2	AE1409	two components res
430	4	50.0	231	2	H72234	uridylylate kinase -
431	4	50.0	231	2	E71678	hypothetical prote
432	4	50.0	231	2	AI3301	glycerone kinase (
433	4	50.0	232	2	T11823	cytochrome-c oxida
434	4	50.0	232	2	T11072	cytochrome-c oxida
435	4	50.0	232	2	T36726	probable regulator
436	4	50.0	233	2	T00566	hypothetical prote
437	4	50.0	233	2	T03329	probable amidase l
438	4	50.0	234	2	S53480	probable membrane
439	4	50.0	234	2	T30427	probable apoptosis
440	4	50.0	235	2	S30482	pol polyprotein -
441	4	50.0	235	2	S30474	pol polyprotein -
442	4	50.0	235	2	S30476	HIV-1 retropepsin
443	4	50.0	236	2	S54428	fimbrial protein h
444	4	50.0	236	2	A75431	hypothetical prote
445	4	50.0	237	2	S26581	heat shock protein
446	4	50.0	237	2	D71182	hypothetical prote
447	4	50.0	237	2	T26765	hypothetical prote
448	4	50.0	237	2	AC0503	conserved hypothet
449	4	50.0	237	2	A75616	phosphoglycerate m
450	4	50.0	238	2	S16578	heat shock protein
451	4	50.0	238	2	AF3023	transcription regu
452	4	50.0	238	2	E81696	hypothetical prote
453	4	50.0	238	2	F70119	antigen, S2 homolo
454	4	50.0	238	2	S60081	transcription regu
455	4	50.0	239	2	E71390	cytochrome-c oxida
456	4	50.0	239	2	AI2773	sugar fermentation
457	4	50.0	239	2	G97553	sugar fermentation
458	4	50.0	239	2	T23038	hypothetical prote
459	4	50.0	239	2	E90234	conserved hypothet
460	4	50.0	240	2	T03379	heat shock protein
461	4	50.0	240	2	A82783	hypothetical prote
462	4	50.0	240	2	S51744	sex-determining pr
463	4	50.0	241	1	S24978	fimbrial protein h
464	4	50.0	241	2	H81384	succinate dehydrog
465	4	50.0	241	2	AC3000	hypothetical prote
466	4	50.0	241	2	T48006	hypothetical prote
467	4	50.0	241	2	T30108	hypothetical prote
468	4	50.0	242	2	E69002	conserved hypothet
469	4	50.0	242	2	C96606	hypothetical prote

470	4	50.0	242	2	AF2543	hypothetical prote
471	4	50.0	243	2	S39497	heat shock protein
472	4	50.0	243	2	A36928	tonB protein - Ent
473	4	50.0	243	2	S28677	hypothetical prote
474	4	50.0	243	2	T10282	late expression fa
475	4	50.0	243	2	D84474	hypothetical prote
476	4	50.0	244	2	S39498	heat shock protein
477	4	50.0	244	2	I36913	beta-myosin heavy
478	4	50.0	244	2	C98261	L-asparagine opero
479	4	50.0	244	2	T15647	hypothetical prote
480	4	50.0	245	2	A71209	hypothetical prote
481	4	50.0	245	2	F84680	hypothetical prote
482	4	50.0	246	2	AB1499	transcription regu
483	4	50.0	246	2	AG1140	transcription regu
484	4	50.0	246	2	C38113	yebC protein - Esc
485	4	50.0	246	2	F90950	hypothetical prote
486	4	50.0	246	2	B85799	hypothetical prote
487	4	50.0	246	2	AG0743	conserved hypothet
488	4	50.0	247	2	S59135	mast cell proteina
489	4	50.0	247	2	S23504	chymase (EC 3.4.21
490	4	50.0	247	2	S64708	chymase (EC 3.4.21
491	4	50.0	247	2	PQ0653	outer capsid spike
492	4	50.0	247	2	PQ0657	outer capsid spike
493	4	50.0	247	2	PQ0658	outer capsid spike
494	4	50.0	247	2	PQ0659	outer capsid spike
495	4	50.0	247	2	PQ0651	outer capsid spike
496	4	50.0	247	2	PQ0661	outer capsid spike
497	4	50.0	247	2	PQ0660	outer capsid spike
498	4	50.0	247	2	PQ0662	outer capsid spike
499	4	50.0	247	2	PQ0652	outer capsid spike
500	4	50.0	247	2	PQ0655	outer capsid spike
501	4	50.0	247	2	PQ0656	outer capsid spike
502	4	50.0	247	2	S61221	outer capsid spike
503	4	50.0	247	2	S61222	outer capsid spike
504	4	50.0	247	2	S61224	outer capsid spike
505	4	50.0	247	2	S73076	hypothetical prote
506	4	50.0	248	2	H90991	probable transcrip
507	4	50.0	248	2	B85837	probable transcrip
508	4	50.0	248	2	D64977	probable transcrip
509	4	50.0	250	1	F65006	hypothetical prote
510	4	50.0	250	2	JC7339	maleate isomerase
511	4	50.0	251	2	T38049	cdp-diacylglycerol
512	4	50.0	251	2	B84016	hypothetical prote
513	4	50.0	252	2	T47263	electron transfer
514	4	50.0	252	2	JC5187	transcription init
515	4	50.0	252	2	D91031	probable chaperone
516	4	50.0	252	2	E85875	probable fimbrial
517	4	50.0	253	2	T12405	cytochrome-c oxida
518	4	50.0	253	2	S07264	beta-crystallin B1
519	4	50.0	253	2	AG2906	hypothetical prote
520	4	50.0	253	2	H97681	heme exporter prot
521	4	50.0	253	2	C84479	probable replicati
522	4	50.0	253	2	AF2428	hypothetical prote
523	4	50.0	254	2	T48732	2,5-diketo-D-gluco
524	4	50.0	254	2	T02854	hypothetical prote
525	4	50.0	254	2	F83271	hypothetical prote
526	4	50.0	254	2	A83821	hypothetical prote

527	4	50.0	255	2	C84224	cytochrome c oxida
528	4	50.0	256	2	E87195	conserved hypothet
529	4	50.0	256	2	T35290	probable transfera
530	4	50.0	257	2	C72418	hypothetical prote
531	4	50.0	257	2	C71265	conserved hypothet
532	4	50.0	258	2	C84758	hypothetical prote
533	4	50.0	259	2	E97233	electron transfer
534	4	50.0	259	2	S32432	toxin cytB - Bacil
535	4	50.0	259	2	T06906	probable ABC-type
536	4	50.0	259	2	T51745	RNA helicase RH16
537	4	50.0	259	2	G83813	phosphatidylserine
538	4	50.0	259	2	AD2926	conserved hypothet
539	4	50.0	259	2	C98356	hypothetical prote
540	4	50.0	260	2	S26043	chymase (EC 3.4.21
541	4	50.0	260	2	D64504	conserved hypothet
542	4	50.0	260	2	H86280	protein F10B6.2 [i
543	4	50.0	262	2	S34609	carboxylesterase (
544	4	50.0	262	2	S76415	hypothetical prote
545	4	50.0	263	2	B43727	cell division init
546	4	50.0	263	2	H85376	hypothetical prote
547	4	50.0	263	2	A84385	hypothetical prote
548	4	50.0	263	2	T04634	hypothetical prote
549	4	50.0	263	2	AI2384	hypothetical prote
550	4	50.0	264	2	E71567	hypothetical prote
551	4	50.0	264	2	AE2787	exopolysaccharide
552	4	50.0	264	2	G97566	exopolysaccharide
553	4	50.0	265	2	D70216	thymidylate syntha
554	4	50.0	267	2	B87578	hypothetical prote
555	4	50.0	267	2	AG1435	PTS system, fructo
556	4	50.0	267	2	AH1077	PTS system, fructo
557	4	50.0	267	2	AE1612	conserved hypothet
558	4	50.0	267	2	T21274	hypothetical prote
559	4	50.0	268	2	D64165	hypothetical prote
560	4	50.0	268	2	D71657	biotin-protein lig
561	4	50.0	268	2	C90056	conserved hypothet
562	4	50.0	268	2	F72547	hypothetical prote
563	4	50.0	268	2	AF0926	probable lipoprote
564	4	50.0	269	2	H71889	phosphomethylpyrim
565	4	50.0	269	2	H75214	hypothetical prote
566	4	50.0	270	2	D64625	thiamin biosynthes
567	4	50.0	270	2	H64433	hypothetical prote
568	4	50.0	270	2	T24529	hypothetical prote
569	4	50.0	273	2	T46108	hypothetical prote
570	4	50.0	273	2	T18809	hypothetical prote
571	4	50.0	274	2	S44616	C08C3.2 protein -
572	4	50.0	275	2	B49394	translation elonga
573	4	50.0	275	2	G75130	translation initia
574	4	50.0	275	2	D71087	probable translati
575	4	50.0	275	2	D69749	transcription regu
576	4	50.0	276	2	E64567	protoporphyrinogen
577	4	50.0	276	2	E71862	protoporphyrinogen
578	4	50.0	277	2	G71822	tRNA delta(2)-isop
579	4	50.0	277	2	T03927	DNA binding protei
580	4	50.0	278	2	C87528	inositol monophosp
581	4	50.0	278	2	F75109	hypothetical prote
582	4	50.0	279	1	S74824	glutamate racemase
583	4	50.0	279	2	T41124	single-stranded DN

584	4	50.0	280	2	T09939	hypothetical prote
585	4	50.0	281	1	A61021	granzyme B (EC 3.4
586	4	50.0	281	2	G83789	lactose transport
587	4	50.0	281	2	S18541	hypothetical prote
588	4	50.0	282	2	T31088	probable rhamnosyl
589	4	50.0	282	2	T26112	hypothetical prote
590	4	50.0	283	2	D75528	exodeoxyribonuclea
591	4	50.0	283	2	E84457	probable mutT doma
592	4	50.0	283	2	T12062	xpsK protein - Xan
593	4	50.0	283	2	B81996	RNA polymerase sig
594	4	50.0	283	2	E81224	RNA polymerase sig
595	4	50.0	284	2	E70232	hypothetical prote
596	4	50.0	284	2	H96613	hypothetical prote
597	4	50.0	284	2	A40689	assemblin, striate
598	4	50.0	286	2	A84063	hypothetical prote
599	4	50.0	287	2	C71207	probable ribose-ph
600	4	50.0	287	2	H64303	coenzyme F420 hydr
601	4	50.0	287	2	T22466	hypothetical prote
602	4	50.0	287	2	AE3578	glycine betaine/l-
603	4	50.0	288	2	S57706	hypothetical prote
604	4	50.0	288	2	S62175	transport vesicle
605	4	50.0	289	2	C36971	outer membrane pho
606	4	50.0	289	2	T40596	probable DNA repai
607	4	50.0	289	2	E90517	methionyl-trna for
608	4	50.0	289	2	G87673	hypothetical prote
609	4	50.0	290	2	H64591	signal peptidase I
610	4	50.0	290	2	T49631	probable Ni-bindin
611	4	50.0	290	2	G86155	hypothetical prote
612	4	50.0	291	2	T31917	hypothetical prote
613	4	50.0	291	2	AI3092	hypothetical prote
614	4	50.0	292	2	S37704	amyD protein - The
615	4	50.0	293	2	D70514	probable oxidoredu
616	4	50.0	293	2	S04649	beta-lactamase (EC
617	4	50.0	293	2	B71215	hypothetical prote
618	4	50.0	293	2	F84028	cell-shape determi
619	4	50.0	293	2	S46710	hypothetical prote
620	4	50.0	293	2	T26934	hypothetical prote
621	4	50.0	294	2	B83040	ribosomal protein
622	4	50.0	294	2	B70034	hypothetical prote
623	4	50.0	294	2	T34199	hypothetical prote
624	4	50.0	294	2	B82254	sodium-type flagel
625	4	50.0	295	2	A42268	biliverdin reducta
626	4	50.0	296	2	A49943	fructose-bisphosph
627	4	50.0	297	2	E81400	polyprenyl synthet
628	4	50.0	297	2	T46864	nicotinate-nucleot
629	4	50.0	298	2	E91229	probable dehydroge
630	4	50.0	298	2	D86076	probable dehydroge
631	4	50.0	298	2	S40826	hypothetical 31.2K
632	4	50.0	298	2	S21389	keratin type II, 6
633	4	50.0	298	2	D71024	hypothetical prote
634	4	50.0	299	2	T02124	hypothetical prote
635	4	50.0	300	2	S76144	hypothetical prote
636	4	50.0	300	2	T43137	hypothetical prote
637	4	50.0	300	2	T32665	hypothetical prote
638	4	50.0	301	1	RLZMRI	rRNA N-glycosidase
639	4	50.0	301	2	A32061	afsA protein - Str
640	4	50.0	301	2	AB3208	transcription regu

641	4	50.0	302	2	A90153	hypothetical prote
642	4	50.0	302	2	G87540	transcription regu
643	4	50.0	303	2	D71300	probable chemotaxi
644	4	50.0	303	2	AE3504	tryptophan synthas
645	4	50.0	303	2	A55136	beta-coat protein
646	4	50.0	303	2	E69670	glycine betaine/ca
647	4	50.0	304	2	A48174	beta-lactamase (EC
648	4	50.0	304	2	H75378	hypothetical prote
649	4	50.0	304	2	F95909	hypothetical prote
650	4	50.0	305	2	H82888	methionyl-tRNA for
651	4	50.0	305	2	E84848	probable RING zinc
652	4	50.0	306	2	C69749	conserved hypothet
653	4	50.0	306	2	T44684	hypothetical prote
654	4	50.0	306	2	T32801	hypothetical prote
655	4	50.0	306	2	E90485	hypothetical prote
656	4	50.0	307	1	B96722	phosphoprotein pho
657	4	50.0	307	2	E86323	protein F14D16.11
658	4	50.0	308	2	G97342	probable ketopanto
659	4	50.0	309	2	AI3000	prephenate dehydro
660	4	50.0	310	2	G98282	tyrC protein [impo
661	4	50.0	311	2	S36619	protein kinase (EC
662	4	50.0	311	2	AF0150	probable outer mem
663	4	50.0	311	2	C75086	methlytransferase
664	4	50.0	311	2	D64240	methionyl-tRNA for
665	4	50.0	311	2	S73625	methionyl-tRNA for
666	4	50.0	311	2	H75411	conserved hypothet
667	4	50.0	311	2	C84101	hypothetical prote
668	4	50.0	312	2	C82356	peptide ABC transp
669	4	50.0	312	2	T32446	hypothetical prote
670	4	50.0	312	2	A89460	protein H42K12.1 [
671	4	50.0	312	2	T33296	hypothetical prote
672	4	50.0	314	1	JC4879	3-hydroxyacyl-CoA
673	4	50.0	314	2	T25842	hypothetical prote
674	4	50.0	314	2	F84143	transposase (10) B
675	4	50.0	314	2	H86354	hypothetical prote
676	4	50.0	314	2	E87427	conserved hypothet
677	4	50.0	314	2	D90349	microsomal dipepti
678	4	50.0	315	2	E71729	proteinase DO (htr
679	4	50.0	315	2	H89797	hypothetical prote
680	4	50.0	315	2	E69400	3-hydroxyacyl-CoA
681	4	50.0	316	2	T50430	conserved hypothet
682	4	50.0	316	2	AC2074	transposase all214
683	4	50.0	317	2	S76723	hypothetical prote
684	4	50.0	317	2	H69620	[acyl-carrier-prot
685	4	50.0	317	2	T41776	BRO-a - Bombyx mor
686	4	50.0	317	2	AD0858	probable secreted
687	4	50.0	318	2	AG1441	phosphoglycerate d
688	4	50.0	318	2	F84495	probable Athila re
689	4	50.0	319	2	S42560	1-aminocyclopropan
690	4	50.0	319	2	S41395	ethylene-forming e
691	4	50.0	319	2	E82178	homoserine O-succi
692	4	50.0	319	2	E86861	methionyl-tRNA for
693	4	50.0	319	2	JC4926	XmnI endonuclease
694	4	50.0	319	2	AB1334	hypothetical prote
695	4	50.0	319	2	AI1704	hypothetical prote
696	4	50.0	320	2	B83238	probable oxidoredu
697	4	50.0	320	2	C72412	fatty acid/phospho



698	4	50.0	320	2	T45909	hypothetical prote
699	4	50.0	320	2	B97206	methyl-accepting c
700	4	50.0	321	2	T34065	hypothetical prote
701	4	50.0	321	2	A82070	transcription regu
702	4	50.0	322	2	D84365	electron transfer
703	4	50.0	322	2	T18966	hypothetical prote
704	4	50.0	322	2	H70462	quinolinate synthe
705	4	50.0	322	2	E71137	hypothetical prote
706	4	50.0	323	2	E71180	probable 3-isoprop
707	4	50.0	323	2	T30380	hypothetical prote
708	4	50.0	323	2	E95864	probable ABC trans
709	4	50.0	324	2	C82214	galactoside ABC tr
710	4	50.0	324	2	A84295	probable DNA helic
711	4	50.0	325	2	F98072	ribosomal protein
712	4	50.0	325	2	F69279	tRNA-pseudouridine
713	4	50.0	325	2	S51569	mocC protein - Rhi
714	4	50.0	325	2	A86202	hypothetical prote
715	4	50.0	326	2	D95197	acetyl xylan ester
716	4	50.0	326	2	A99064	xylan esterase 1 (
717	4	50.0	326	2	T52030	gamma-glutamyl hyd
718	4	50.0	326	2	F69360	adenosylhomocystei
719	4	50.0	327	2	F96815	hypothetical prote
720	4	50.0	329	2	S49490	MAPK-activated pro
721	4	50.0	329	2	F70156	conserved hypothet
722	4	50.0	330	1	RNECKF	transcription init
723	4	50.0	330	1	QQBEP7	gene 62 protein -
724	4	50.0	330	2	E75535	malate dehydrogena
725	4	50.0	330	2	S47534	transcription init
726	4	50.0	330	2	S49471	transcription init
727	4	50.0	330	2	C91078	sigma factor RpoS
728	4	50.0	330	2	D85923	hypothetical prote
729	4	50.0	330	2	AG0855	RNA polymerase sig
730	4	50.0	330	2	T42975	hypothetical prote
731	4	50.0	330	2	A87194	polyprenyl diphosp
732	4	50.0	330	2	H95166	transcription regu
733	4	50.0	330	2	T48100	tRNA isopentenyl t
734	4	50.0	330	2	G98032	hypothetical prote
735	4	50.0	331	2	B55552	trans-o-hydrobenzy
736	4	50.0	331	2	G84646	hypothetical prote
737	4	50.0	331	2	AB2439	UDP-N-acetylenolpy
738	4	50.0	332	1	JGECG	D-galactose-bindin
739	4	50.0	332	1	S15554	D-galactose-bindin
740	4	50.0	332	1	S29390	galactose-binding
741	4	50.0	332	1	B39136	flagellar motor sw
742	4	50.0	332	2	T12433	malate dehydrogena
743	4	50.0	332	2	T02935	malate dehydrogena
744	4	50.0	332	2	B91009	galactose-binding
745	4	50.0	332	2	D85853	galactose-binding
746	4	50.0	332	2	AF0781	D-galactose-bindin
747	4	50.0	332	2	T21182	hypothetical prote
748	4	50.0	332	2	G64141	probable tetraacyl
749	4	50.0	332	2	T45770	hypothetical prote
750	4	50.0	332	2	T19457	hypothetical prote
751	4	50.0	333	1	DELOG3	glyceraldehyde-3-p
752	4	50.0	333	2	D75067	probable dehydroge
753	4	50.0	333	2	B64085	glpX protein - Hae
754	4	50.0	333	2	G95401	TRm24 probable tra



755	4	50.0	333	2	H95304	TRm24 transposase
756	4	50.0	333	2	H95327	TRm24 transposase
757	4	50.0	333	2	E89797	hypothetical prote
758	4	50.0	333	2	S22643	integrase - Mycoba
759	4	50.0	333	2	T33311	hypothetical prote
760	4	50.0	333	2	A83797	protein secretion
761	4	50.0	334	2	T22427	hypothetical prote
762	4	50.0	334	2	G86723	exodeoxyribonuclea
763	4	50.0	334	2	JC4870	pepsin A (EC 3.4.2
764	4	50.0	334	2	H49343	probable trans-o-h
765	4	50.0	334	2	D83750	pyridoxal phosphat
766	4	50.0	334	2	B69888	GTP-binding protei
767	4	50.0	334	2	T29672	hypothetical prote
768	4	50.0	334	2	T02674	hypothetical prote
769	4	50.0	335	1	D65106	hypothetical 37.1
770	4	50.0	335	2	AG0183	galactose-binding
771	4	50.0	335	2	A91134	probable enzyme [i
772	4	50.0	335	2	D85979	probable enzyme yh
773	4	50.0	335	2	AH0900	probable monooxyge
774	4	50.0	335	2	F64043	[citrate (pro-3S)-
775	4	50.0	335	2	T41354	nucleoporin GLFG h
776	4	50.0	336	2	S30972	minor tail protein
777	4	50.0	337	2	A54214	C 4.2.3.7 pentalen
778	4	50.0	337	2	B69356	hypothetical prote
779	4	50.0	337	2	T31711	hypothetical prote
780	4	50.0	338	2	T36025	conserved hypothet
781	4	50.0	338	2	AG2298	hypothetical prote
782	4	50.0	339	2	A64122	dihydroorotate oxi
783	4	50.0	339	2	T25204	hypothetical prote
784	4	50.0	340	2	A71669	dna-directed RNA p
785	4	50.0	340	2	F97822	hypothetical prote
786	4	50.0	340	2	C69328	iron-sulfur cluste
787	4	50.0	340	2	T14921	probable lipoprote
788	4	50.0	341	1	H69401	probable radical-f
789	4	50.0	341	2	T01538	receptor-like prot
790	4	50.0	341	2	S52527	hypothetical prote
791	4	50.0	341	2	H71716	190 kd antigen pre
792	4	50.0	341	2	T08459	hypothetical prote
793	4	50.0	341	2	T48847	syntaxin synt4 [im
794	4	50.0	341	2	AB3002	conserved hypothet
795	4	50.0	341	2	F98281	hypothetical prote
796	4	50.0	342	1	S64322	probable membrane
797	4	50.0	342	2	T29245	hypothetical prote
798	4	50.0	342	2	H86300	F19K19.12 protein
799	4	50.0	342	2	T45227	probable F420H2-de
800	4	50.0	342	2	T22742	hypothetical prote
801	4	50.0	343	2	AB1086	ATP synthase delta
802	4	50.0	343	2	G90680	probable periplasm
803	4	50.0	343	2	C85531	periplasmic ferric
804	4	50.0	344	2	E95868	probable epoxide h
805	4	50.0	344	2	F81911	probable phosphori
806	4	50.0	344	2	E81104	phosphoribosylform
807	4	50.0	344	2	B84242	hypothetical prote
808	4	50.0	344	2	S46745	hypothetical prote
809	4	50.0	344	2	T27119	hypothetical prote
810	4	50.0	344	2	T51329	DNA binding protei
811	4	50.0	344	2	T23113	hypothetical prote

812	4	50.0	344	2	AB1558	conserved hypothet
813	4	50.0	344	2	AD1200	conserved hypothet
814	4	50.0	346	2	B75160	3-isopropylmalate
815	4	50.0	346	2	S34165	keratin, type II -
816	4	50.0	346	2	A48470	translation elonga
817	4	50.0	346	2	B84602	probable DnaJ prot
818	4	50.0	347	2	C87281	hypothetical prote
819	4	50.0	347	2	T24175	hypothetical prote
820	4	50.0	348	2	T24016	hypothetical prote
821	4	50.0	348	2	C91060	hypothetical prote
822	4	50.0	349	2	T03500	hypothetical prote
823	4	50.0	349	2	AB3094	conserved hypothet
824	4	50.0	349	2	H98192	hypothetical prote
825	4	50.0	350	2	AG3425	iolE protein [impo
826	4	50.0	350	2	AE2954	conserved hypothet
827	4	50.0	351	2	T41572	hypothetical prote
828	4	50.0	351	2	A88103	protein W10G11.7 [
829	4	50.0	351	2	E87451	conserved hypothet
830	4	50.0	351	2	AF2844	hypothetical prote
831	4	50.0	351	2	H97621	lipopolysaccharide
832	4	50.0	352	2	F83617	hypothetical prote
833	4	50.0	353	2	H75020	hypothetical prote
834	4	50.0	353	2	F84252	phycocyanin alpha
835	4	50.0	354	2	AH0009	methyated-DNA-[pr
836	4	50.0	354	2	AG0617	probable bacteriop
837	4	50.0	354	2	C69755	hypothetical prote
838	4	50.0	355	2	D84192	glutamate decarbox
839	4	50.0	356	1	A71089	probable dipeptida
840	4	50.0	356	2	S49011	yolk protein 2 - b
841	4	50.0	356	2	H72803	integrase protein
842	4	50.0	357	2	S23525	cinnamyl-alcohol d
843	4	50.0	357	2	S23526	cinnamyl-alcohol d
844	4	50.0	357	2	T05413	cinnamyl-alcohol d
845	4	50.0	357	2	C82554	conserved hypothet
846	4	50.0	357	2	T01571	hypothetical prote
847	4	50.0	357	2	A96194	hypothetical prote
848	4	50.0	358	2	T11165	ubiquinol-cytochro
849	4	50.0	358	2	AE2218	hypothetical prote
850	4	50.0	358	2	D96579	hypothetical prote
851	4	50.0	359	2	B96697	protein F1N21.20 [
852	4	50.0	359	2	JC7996	36K chitinase (EC
853	4	50.0	360	1	S30109	D-vitopine dehydro
854	4	50.0	360	2	D69623	flagellar biosynth
855	4	50.0	360	2	AI2829	conserved hypothet
856	4	50.0	361	2	T13745	hypothetical prote
857	4	50.0	361	2	F72862	hypothetical prote
858	4	50.0	361	2	B59099	hypothetical prote
859	4	50.0	362	2	T09886	hypothetical prote
860	4	50.0	363	2	I40234	carboxymethylcellu
861	4	50.0	363	2	G83954	flagella-associate
862	4	50.0	363	2	F87754	protein C43E11.1 [
863	4	50.0	363	2	F84360	threonine synthase
864	4	50.0	363	2	T27388	hypothetical prote
865	4	50.0	364	2	S69885	H+-transporting tw
866	4	50.0	364	2	E72512	probable tyrosyl-t
867	4	50.0	364	2	AB1918	hypothetical prote
868	4	50.0	365	2	C86746	peptide chain rele

869	4	50.0	366	2	E72400	DNA polymerase III
870	4	50.0	366	2	T16249	hypothetical prote
871	4	50.0	366	2	S46736	hypothetical prote
872	4	50.0	367	2	A70018	multiple sugar ABC
873	4	50.0	368	2	AI1291	glycerol dehydroge
874	4	50.0	368	2	S48487	hypothetical prote
875	4	50.0	369	2	S74983	hypothetical prote
876	4	50.0	369	2	S68692	deoxyhypusine synt
877	4	50.0	369	2	AC2665	conserved hypothet
878	4	50.0	370	2	JC2204	MAPK-activated pro
879	4	50.0	370	2	H98328	hypothetical prote
880	4	50.0	371	1	A43830	alanine dehydrogen
881	4	50.0	371	2	F87100	L-alanine dehydrog
882	4	50.0	371	2	C84254	hypothetical prote
883	4	50.0	371	2	F69429	asparagine synthet
884	4	50.0	372	2	H69426	probable transamin
885	4	50.0	374	2	H81399	2-oxoglutarate-fer
886	4	50.0	374	2	S76392	phosphoglycerate k
887	4	50.0	374	2	AF1280	probable exonuclea
888	4	50.0	374	2	AF1643	probable exonuclea
889	4	50.0	375	2	E85035	hypothetical prote
890	4	50.0	376	1	JQ0474	alcohol dehydrogen
891	4	50.0	376	2	C84316	hypothetical prote
892	4	50.0	376	2	AF2289	hypothetical prote
893	4	50.0	377	2	T12042	cysteine proteinas
894	4	50.0	377	2	A90482	conserved hypothet
895	4	50.0	378	2	T30435	very late factor 1
896	4	50.0	378	2	T50090	hypothetical prote
897	4	50.0	378	2	D83945	hypothetical prote
898	4	50.0	379	1	S04571	alcohol dehydrogen
899	4	50.0	379	1	DEILSP	alcohol dehydrogen
900	4	50.0	379	1	S01893	alcohol dehydrogen
901	4	50.0	379	2	T50969	probable DELTA(24)
902	4	50.0	379	2	A82101	lipid-A-disacchari
903	4	50.0	379	2	H82284	queueine tRNA-ribos
904	4	50.0	379	2	C84253	hypothetical prote
905	4	50.0	381	1	KIRBCB	creatine kinase (E
906	4	50.0	381	2	T45940	hypothetical prote
907	4	50.0	381	2	T20890	hypothetical prote
908	4	50.0	382	1	I39848	cell division init
909	4	50.0	382	2	AD2981	isomerase/lactoniz
910	4	50.0	383	1	RDECLA	lactaldehyde reduc
911	4	50.0	383	2	C91086	L-1,2-propanediol
912	4	50.0	383	2	E85931	L-1,2-propanediol
913	4	50.0	383	2	JC2472	brain and reproduc
914	4	50.0	383	2	C70845	probable nagA prot
915	4	50.0	384	2	S58446	sigma S - Salmonel
916	4	50.0	384	2	T50921	carbamoyl-phosphat
917	4	50.0	384	2	AI1843	hypothetical prote
918	4	50.0	384	2	S45592	ERD1 protein - yea
919	4	50.0	384	2	D87471	ROK family protein
920	4	50.0	384	2	D69548	conserved hypothet
921	4	50.0	385	2	G83817	coproporphyrinogen
922	4	50.0	385	2	S78100	MAPK-activated pro
923	4	50.0	385	2	G72659	probable type II D
924	4	50.0	385	2	C90368	proteinase, probab
925	4	50.0	385	2	T23980	hypothetical prote

926	4	50.0	386	2	H71701	succinyl-CoA synth
927	4	50.0	386	2	G97774	succinate-CoA liga
928	4	50.0	386	2	T26108	hypothetical prote
929	4	50.0	387	2	H71708	pol (A) POLYMERASE
930	4	50.0	387	2	T38876	probable ribosomal
931	4	50.0	387	2	C71827	hypothetical prote
932	4	50.0	387	2	E64688	hypothetical prote
933	4	50.0	387	2	A47446	HNF-3/fork head fa
934	4	50.0	387	2	A86322	F6A14.9 protein -
935	4	50.0	388	2	D84962	tryptophan synthas
936	4	50.0	388	2	F70133	flagellar-associat
937	4	50.0	388	2	AF1162	hypothetical prote
938	4	50.0	388	2	AF1521	hypothetical prote
939	4	50.0	388	2	A87701	citrate synthase [
940	4	50.0	389	2	D90248	DNA topoisomerase
941	4	50.0	389	2	G84245	NADH dehydrogenase
942	4	50.0	389	2	T04390	NBS-LRR type resis
943	4	50.0	390	2	T41199	dom34 protein homo
944	4	50.0	390	2	C69276	coenzyme F420-quin
945	4	50.0	392	2	T38450	probable GTP-bindi
946	4	50.0	392	2	G84191	hypothetical prote
947	4	50.0	392	2	T25474	hypothetical prote
948	4	50.0	392	2	H97335	Na+ ABC transporte
949	4	50.0	393	2	T02069	probable DNA-bindi
950	4	50.0	393	2	T25908	hypothetical prote
951	4	50.0	393	2	S48381	RRD1 protein - yea
952	4	50.0	393	2	B97447	hypothetical prote
953	4	50.0	394	2	T20868	hypothetical prote
954	4	50.0	395	2	T47122	cell division prot
955	4	50.0	395	2	G75046	pyruvate synthase
956	4	50.0	395	2	A86458	probable elicitor
957	4	50.0	395	2	T22692	hypothetical prote
958	4	50.0	395	2	T31578	hypothetical prote
959	4	50.0	396	2	S39793	MAPK-activated pro
960	4	50.0	396	2	G87651	phosphoglycerate k
961	4	50.0	396	2	A34401	cathepsin E (EC 3.
962	4	50.0	396	2	C84394	argininosuccinate
963	4	50.0	396	2	S58161	probable translati
964	4	50.0	396	2	T45088	pyruvate synthase
965	4	50.0	397	1	A47489	4-hydroxybenzoate
966	4	50.0	397	2	S70987	dnaN protein - Myc
967	4	50.0	398	2	E71114	probable ferredoxi
968	4	50.0	398	2	B86353	protein F2E2.6 [im
969	4	50.0	399	2	T10002	DNA-directed DNA p
970	4	50.0	399	2	E71169	hypothetical prote
971	4	50.0	400	2	A39495	NADPH2 dehydrogena
972	4	50.0	400	2	G69143	conserved hypothet
973	4	50.0	401	2	A86251	hypothetical prote
974	4	50.0	402	1	BOHUS	sex steroid-bindin
975	4	50.0	402	2	F70850	DNA-directed DNA p
976	4	50.0	402	2	S58477	rds1 protein - fis
977	4	50.0	404	2	AI3350	isocitrate dehydro
978	4	50.0	404	2	T09606	probable LFY flora
979	4	50.0	404	2	AB2188	hypothetical prote
980	4	50.0	405	2	H75085	probable RNA methy
981	4	50.0	405	2	T29639	hypothetical prote
982	4	50.0	405	2	D75135	hypothetical prote

983	4	50.0	406	2	JC4600	isocitrate dehydro
984	4	50.0	406	2	AF2631	hypothetical prote
985	4	50.0	406	2	B89942	conserved hypothet
986	4	50.0	407	2	T41708	gtp binding protei
987	4	50.0	407	2	H97413	hypothetical prote
988	4	50.0	407	2	D98302	hypothetical prote
989	4	50.0	408	2	C86799	hypothetical prote
990	4	50.0	409	2	PN0007	phosphoglycerate k
991	4	50.0	409	2	A84733	hypothetical prote
992	4	50.0	410	1	I40755	trigger factor 2 [
993	4	50.0	410	2	AD2553	hypothetical prote
994	4	50.0	411	2	H69139	hypothetical prote
995	4	50.0	411	2	T15705	hypothetical prote
996	4	50.0	412	2	C88923	protein W03F9.1 [i
997	4	50.0	412	2	T15214	hypothetical prote
998	4	50.0	412	2	F87624	peptidase, M20/M25
999	4	50.0	412	2	C96816	hypothetical prote
1000	4	50.0	412	2	T40295	fructosyl amine -

# ALIGNMENTS

## RESULT 1

S23094

beta-amyloid protein precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-May-1996

C;Accession: S23094

R;Kojima, S.; Omori, M.

FEBS Lett. 304, 57-60, 1992

A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase.

A;Reference number: S23094; MUID:92316198; PMID:1618299

A;Accession: S23094

A;Molecule type: protein

A;Residues: 1-33 <KOJ>

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 100.0%; Score 8; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 0.0062;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 2 EVKMDAEF 9

## RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C;Species: Ovis sp. (sheep)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: E60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: E60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56130

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 8; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.0095;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

#### RESULT 3

F60045

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C;Accession: F60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: F60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 8; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.0095;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

#### RESULT 4

G60045

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: G60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: G60045  
 A;Molecule type: mRNA  
 A;Residues: 1-57 <JOH>  
 A;Cross-references: EMBL:X56126  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 8; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

#### RESULT 5

D60045

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: D60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: D60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56124

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 8; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

#### RESULT 6

A60045

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)

C;Species: Canis lupus familiaris (dog)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995

C;Accession: A60045



R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide  
 in dog, polar bear and five other mammals by cross-species polymerase chain  
 reaction analysis.  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: A60045  
 A;Molecule type: mRNA  
 A;Residues: 1-57 <JOH>  
 A;Cross-references: EMBL:X56125  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type  
 proteinase inhibitor homology  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 8; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

#### RESULT 7

B60045

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)

C;Species: Ursus maritimus (polar bear)

C;Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999

C;Accession: B60045

R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide  
 in dog, polar bear and five other mammals by cross-species polymerase chain  
 reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157

A;Accession: B60045

A;Molecule type: mRNA

A;Residues: 1-57 <JOH>

A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type  
 proteinase inhibitor homology

C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 8; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.0095;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

#### RESULT 8

PQ0438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995

C;Accession: PQ0438; C60045  
 R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.  
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
 A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor protein gene.  
 A;Reference number: PQ0438; MUID:93075180; PMID:1445331  
 A;Accession: PQ0438  
 A;Molecule type: DNA  
 A;Residues: 1-82 <DAV>  
 A;Cross-references: GB:M83558; GB:M83657  
 R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
 Brain Res. Mol. Brain Res. 10, 299-305, 1991  
 A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.  
 A;Reference number: A60045; MUID:92017079; PMID:1656157  
 A;Accession: C60045  
 A;Molecule type: mRNA  
 A;Residues: 12-68 <JOH>  
 A;Cross-references: EMBL:X56129  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology  
 C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 8; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 13 EVKMDAEF 20

# RESULT 9

A49795  
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
 C;Species: Macaca fascicularis (crab-eating macaque)  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C;Accession: A49795  
 R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.  
 Am. J. Pathol. 138, 1423-1435, 1991  
 A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.  
 A;Reference number: A49795; MUID:91273117; PMID:1905108  
 A;Accession: A49795  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-695 <POD>  
 A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063  
 C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology  
 C;Keywords: alternative splicing

Query Match 100.0%; Score 8; DB 1; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.066;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 593 EVKMDAEF 600

RESULT 10

A27485

Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;Alternate names: proteinase nexin II

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 13-Aug-1999

C;Accession: A27485; S19727; I49485

R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.

Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.

A;Reference number: A27485; MUID:88106489; PMID:3322280

A;Accession: A27485

A;Molecule type: mRNA

A;Residues: 1-695 <YAM>

A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085

A;Experimental source: brain

R;de Strooper, B.; van Leuven, F.; van den Berghe, H.

Biochim. Biophys. Acta 1129, 141-143, 1991

A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.

A;Reference number: S19727; MUID:92096458; PMID:1756177

A;Accession: S19727

A;Molecule type: mRNA

A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695  
<STR>

A;Cross-references: EMBL:X59379

R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.

Gene 112, 189-195, 1992

A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.

A;Reference number: I49485; MUID:92209998; PMID:1555768

A;Accession: I49485

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-19 <RES>

A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329

C;Genetics:

A;Map position: 16C3

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 8; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.066;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 593 EVKMDAEF 600

RESULT 11

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N;Alternate names: beta-A4 amyloid protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 13-Aug-1999

C;Accession: S00550; A41245; A39820; S46251

R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.

EMBO J. 7, 1365-1370, 1988

A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.

A;Reference number: S00550; MUID:88312583; PMID:2900758

A;Accession: S00550

A;Molecule type: mRNA

A;Residues: 1-695 <SHI>

A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617

R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.

Science 241, 223-226, 1988

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.

A;Reference number: A41245; MUID:88264430; PMID:2968652

A;Accession: A41245

A;Molecule type: protein

A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>

A;Note: evidence for heparan sulfate attachment

R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.

FEBS Lett. 349, 109-116, 1994

A;Title: The beta-A4 amyloid precursor protein binding to copper.

A;Reference number: S46251; MUID:94320627; PMID:7913895

A;Contents: annotation; copper binding sites

A;Note: rat peptides were isolated but not sequenced

R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.

J. Biol. Chem. 266, 8464-8469, 1991

A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.

A;Reference number: A39820; MUID:91217087; PMID:1673681

A;Accession: A39820

A;Status: preliminary

A;Molecule type: protein

A;Residues: 18-32 <POT>

A;Experimental source: brain

C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of both Alzheimer's disease and Down's syndrome.

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein

F;625-648/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 8; DB 2; Length 695;

Best Local Similarity 100.0%; Pred. No. 0.066;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 593 EVKMDAEF 600

RESULT 12

QRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)

N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038; S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644  
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.

Nucleic Acids Res. 17, 517-522, 1989

A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.

A;Reference number: S02260; MUID:89128427; PMID:2783775

A;Accession: S02260

A;Molecule type: DNA

A;Residues: 1-288, 'V', 365-770 <LEM1>

A;Cross-references: EMBL:X13466

A;Note: alternative splice form APP(695)

R;Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A;Reference number: S05194

A;Accession: S05194

A;Molecule type: DNA

A;Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>

A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360

A;Note: alternative splice form APP(695)

R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.

A;Reference number: A32277; MUID:89165870; PMID:2538123

A;Accession: A32277

A;Molecule type: DNA

A;Residues: 1-75 <LAF>

A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074

R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.

A;Reference number: A33260; MUID:89392030; PMID:2675837

A;Accession: A33260

A;Molecule type: DNA

A;Residues: 656-737 <JOH>

A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865

R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.

A;Reference number: A35486; MUID:90321244; PMID:2196878

A;Accession: A35486

A;Molecule type: DNA

A;Residues: 672-710 <PRE1>

A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients

R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y. Gene 87, 257-263, 1990

A;Title: Genomic organization of the human amyloid beta-protein precursor gene.

A;Reference number: I39451; MUID:90236318; PMID:2110105

A;Accession: I39452

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-770 <YOS1>

A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616

A;Accession: I39451

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>

A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615

R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y. Gene 102, 291-292, 1991

A;Reference number: A59020; MUID:91340168; PMID:1908403

A;Contents: annotation; erratum

A;Note: revised physical map for reference I39451

R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B. Science 248, 1124-1126, 1990

A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.

A;Reference number: I39453; MUID:90260663; PMID:2111584

A;Accession: I39453

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 656-737 <LEV>

A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620

A;Note: a mutation with 693-Gln is presented

R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D. Science 254, 97-99, 1991

A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.

A;Reference number: I59562; MUID:92022553; PMID:1925564

A;Accession: I59562

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 689-716, 'F', 718-737 <MUR>

A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721

R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.



Am. J. Hum. Genet. 51, 998-1014, 1992

A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.

A;Reference number: A44017; MUID:93035397; PMID:1415269

A;Accession: A44017

A;Molecule type: DNA

A;Residues: 687-692,'G',694-718 <KAM1>

A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378

A;Experimental source: familial Alzheimer disease family SB

A;Note: sequence extracted from NCBI backbone (NCBIP:115374)

A;Accession: B44017

A;Molecule type: DNA

A;Residues: 687-718 <KAM2>

A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380

A;Experimental source: familial Alzheimer disease family LIT

A;Note: sequence extracted from NCBI backbone (NCBIP:115376)

A;Note: this sequence has a silent mutation

R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B. Nature 325, 733-736, 1987

A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.

A;Reference number: A03134; MUID:87144572; PMID:2881207

A;Accession: A03134

A;Molecule type: mRNA

A;Residues: 1-288,'V',365-770 <KAN>

A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526

A;Note: alternative splice form APP(695)

R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M. Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.

A;Reference number: A29030; MUID:87231971; PMID:3035574

A;Accession: A29030

A;Molecule type: mRNA

A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>

A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540

A;Note: the authors translated the codon GAG for residue 647 as Asp

R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C. Science 235, 877-880, 1987

A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.

A;Reference number: A47584; MUID:87120328; PMID:3810169

A;Accession: A47584

A;Molecule type: mRNA

A;Residues: 674-756,'S',758-770 <GOL>

A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707

A;Experimental source: brain

R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L. Science 235, 880-884, 1987

A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.

A;Reference number: A47585; MUID:87120329; PMID:2949367

A;Accession: A47585

A;Molecule type: mRNA

A;Residues: 674-703 <TAN1>



A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958  
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.  
 EMBO J. 7, 949-957, 1988  
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.  
 A;Reference number: S02638; MUID:88296437; PMID:2900137  
 A;Accession: S02638  
 A;Molecule type: mRNA  
 A;Residues: 672-678 <DYZ>  
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.  
 Nature 331, 528-530, 1988  
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.  
 A;Reference number: S00707; MUID:88122640; PMID:2893290  
 A;Accession: S00707  
 A;Molecule type: mRNA  
 A;Residues: 286-344, 'I', 365-366 <TAN2>  
 A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612  
 A;Experimental source: promyelocytic leukemia cell line HL60  
 A;Note: alternative splice form APP(751)  
 R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.  
 Nature 331, 525-527, 1988  
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.  
 A;Reference number: S00925; MUID:88122639; PMID:2893289  
 A;Accession: S00925  
 A;Molecule type: mRNA  
 A;Residues: 1-344, 'I', 365-770 <PO2>  
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721  
 A;Note: alternative splice form APP(751)  
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
 Nature 331, 530-532, 1988  
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.  
 A;Reference number: A38949; MUID:88122641; PMID:2893291  
 A;Accession: A38949  
 A;Molecule type: mRNA  
 A;Residues: 287-367 <KIT>  
 A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611  
 A;Experimental source: glioblastoma cell line  
 A;Note: alternative splice form APP(770)  
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.  
 Brain Res. Mol. Brain Res. 4, 121-131, 1988  
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.  
 A;Reference number: A30320  
 A;Accession: A30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 284-288, 'V', 365-770 <VIT1>  
 A;Accession: B30320  
 A;Status: not compared with conceptual translation

A;Molecule type: mRNA  
 A;Residues: 122-288,'V',365-770 <VIT2>  
 A;Accession: C30320  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 606-770 <VIT3>  
 R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.;  
 Marotta, C.A.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
 A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 disease brain: coding and noncoding regions of the fetal precursor mRNA are  
 expressed in the cortex.  
 A;Reference number: A31087; MUID:88124954; PMID:2893379  
 A;Accession: A31087  
 A;Molecule type: mRNA  
 A;Residues: 507-770 <ZAI>  
 A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573  
 A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for  
 residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT  
 for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn,  
 AAT for residue 610 as Gly, and GGT for residue 655 as Ser  
 A;Note: the cited Genbank accession number, J03594, is not in release 101.0  
 R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.;  
 Beyreuther, K.

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.072;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
 |||||  
 Db 668 EVKMDAEF 675

# RESULT 13

T27174

hypothetical protein Y54G11A.11 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T27174

R;Wallis, J.

submitted to the EMBL Data Library, December 1998

A;Reference number: Z20322

A;Accession: T27174

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-84 <WIL>

A;Cross-references: EMBL:AL034488; NID:e1359895; PIDN:CAA22454.1;  
 CESP:Y54G11A.11

A;Experimental source: clone Y54G11A

C;Genetics:

A;Gene: CESP:Y54G11A.11

A;Introns: 39/2

Query Match 62.5%; Score 5; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            1 EVKMD 5  
              | | | |  
Db            36 EVKMD 40

RESULT 14

PH1526

gamma-aminobutyric acid receptor NB4.1 - fruit fly (*Drosophila* sp.) (fragments)  
C;Species: *Drosophila* sp.  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PH1526  
R;Ffrench-Constant, R.H.; Rocheleau, T.A.  
J. Neurochem. 60, 2323-2326, 1993  
A;Title: *Drosophila* gamma-aminobutyric acid receptor gene *Rdl* shows extensive alternative splicing.  
A;Reference number: PH1526; MUID:93260477; PMID:7684073  
A;Accession: PH1526  
A;Molecule type: mRNA  
A;Residues: 1-44,45-105 <FFR>  
A;Experimental source: embryo  
C;Genetics:  
A;Gene: *Rdl*  
A;Cross-references: FlyBase:FBgn0004244  
C;Superfamily: acetylcholine receptor  
C;Keywords: alternative splicing; receptor

Query Match                    62.5%;    Score 5;    DB 2;    Length 105;  
Best Local Similarity    100.0%;    Pred. No. 44;  
Matches       5;    Conservative       0;    Mismatches       0;    Indels       0;    Gaps       0;

Qy            1 EVKMD 5  
              | | | |  
Db            30 EVKMD 34

RESULT 15

H90315

conserved hypothetical protein [imported] - *Sulfolobus solfataricus*  
C;Species: *Sulfolobus solfataricus*  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C;Accession: H90315  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Weiher, C.C.Y.; Clausen, I.G.; Curtis, B.A.; De Moors, A.; Erauso, G.; Fletcher, C.; Gordon, P.M.K.; Heikamp-de Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; Schenk, M.E.; Theriault, C.; Tolstrup, N.; Charlebois, R.L.; Doolittle, W.F.; Duguet, M.; Gaasterland, T.; Garrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: *Sulfolobus solfataricus* complete genome.  
A;Reference number: A99139  
A;Accession: H90315  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-127 <KUR>  
A;Cross-references: GB:AE006641; NID:g13814799; PIDN:AAK41783.1; GSPDB:GN00155  
C;Genetics:

A;Gene: SS01570

Query Match 62.5%; Score 5; DB 2; Length 127;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 11 EVKMD 15

RESULT 16

T21857

hypothetical protein F36D3.10 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T21857

R;McMurray, A.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19478

A;Accession: T21857

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-140 <WIL>

A;Cross-references: EMBL:Z81531; PIDN:CAB04323.1; GSPDB:GN00023; CESP:F36D3.10

A;Experimental source: clone F36D3

C;Genetics:

A;Gene: CESP:F36D3.10

A;Map position: 5

A;Introns: 24/3; 46/3; 87/3

Query Match 62.5%; Score 5; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 55 KMDAE 59

RESULT 17

C69136

hypothetical protein MTH286 - *Methanobacterium thermoautotrophicum* (strain Delta H)

C;Species: *Methanobacterium thermoautotrophicum*

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999

C;Accession: C69136

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.;  
Aldredge, T.; Bashirzadeh, R.; Blakely, D.; Cook, R.; Gilbert, K.; Harrison, D.;  
Hoang, L.; Keagle, P.; Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire,  
R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso, A.; Bush, D.;  
Safer, H.; Patwell, D.; Prabhakar, S.; McDougall, S.; Shimer, G.; Goyal, A.;  
Pietrokovski, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.;  
Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: functional analysis and comparative genomics.

A;Reference number: A69000; MUID:98037514; PMID:9371463  
A;Accession: C69136  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-146 <MTH>  
A;Cross-references: GB:AE000814; GB:AE000666; NID:g2621334; PIDN:AAB84792.1;  
PID:g2621338  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH286  
A;Start codon: GTG  
C;Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH286

Query Match 62.5%; Score 5; DB 2; Length 146;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 129 EVKMD 133

#### RESULT 18

A95928  
probable amine oxidase (flavin-containing) (EC 1.4.3.4) [imported] -  
Sinorhizobium meliloti (strain 1021) megaplasmid pSymB  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 14-Sep-2001  
C;Accession: A95928  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Becker, A.; Cowie, A.; Gouzy, J.; Golding, B.; Puhler, A.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: A95928  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-153 <KUR>  
A;Cross-references: GB:AL591985; PIDN:CAC49089.1; PID:g15140574; GSPDB:GN00167  
A;Experimental source: strain 1021, megaplasmid pSymB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.; Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.; Huizar, L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Ramsperger, U.; Surzycki, R.; Thebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:

A;Gene: SMb21110  
A;Genome: plasmid  
C;Superfamily: maoC protein  
C;Keywords: oxidoreductase

Query Match 62.5%; Score 5; DB 2; Length 153;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8  
|||||  
Db 44 MDAEF 48

RESULT 19

S73644

hypothetical protein G12\_orf168 - Mycoplasma pneumoniae (strain ATCC 29342)

C;Species: Mycoplasma pneumoniae

A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999

C;Accession: S73644

R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73644

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-168 <HIM>

A;Cross-references: EMBL:AE000029; GB:U00089; NID:g1673986; PIDN:AAB95966.1;  
PID:g1673991

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics:

A;Genetic code: SGC3

C;Superfamily: conserved hypothetical protein C09\_orf180

Query Match 62.5%; Score 5; DB 2; Length 168;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 124 EVKMD 128

RESULT 20

C95230

hypothetical protein SP1969 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001

C;Accession: C95230

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.;

Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001  
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.  
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
 A;Reference number: A95000; MUID:21357209; PMID:11463916  
 A;Accession: C95230  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-179 <KUR>  
 A;Cross-references: GB:AE005672; PIDN:AAK76036.1; PID:g14973476; GSPDB:GN00164; TIGR:SP4SP1969  
 A;Experimental source: strain TIGR4  
 C;Genetics:  
 A;Gene: SP1969  
 C;Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nikA intergenic region)

Query Match 62.5%; Score 5; DB 2; Length 179;  
 Best Local Similarity 100.0%; Pred. No. 66;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KMDAE 7  
 |||||  
 Db 97 KMDAE 101

# RESULT 21

F98094

conserved hypothetical protein spr1784 [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001

C;Accession: F98094

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Estrem, S.; Fritz, L.; Fu, D.J.; Fuller, W.; Geringer, C.; Gilmour, R.; Glass, J.S.; Khoja, H.; Kraft, A.; LaGace, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McHenney, M.; McLeaster, K.; Mundy, C.; Nicas, T.I.; Norris, F.H.; O'Gara, M.; Peery, R.; Robertson, G.T.; Rockey, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Rosteck Jr., P.R.; Skatrud, P.L.; Glass, J.I.

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: F98094

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-179 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAL00587.1; PID:g15459468; GSPDB:GN00174

C;Genetics:

A;Gene: spr1784

C;Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nikA intergenic region)



Query Match 62.5%; Score 5; DB 2; Length 179;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 97 KMDAE 101

RESULT 22

S73668

hypothetical protein P02\_orf196 - Mycoplasma pneumoniae (strain ATCC 29342)

C;Species: Mycoplasma pneumoniae

A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999

C;Accession: S73668

R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73668

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-196 <HIM>

A;Cross-references: EMBL:AE000032; GB:U00089; NID:g1674011; PIDN:AAB95989.1;  
PID:g1674017

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics:

A;Genetic code: SGC3

C;Superfamily: conserved hypothetical protein C09\_orf180

Query Match 62.5%; Score 5; DB 2; Length 196;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 166 EVKMD 170

RESULT 23

T11657

rho GDP dissociation inhibitor. - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2000

C;Accession: T11657

R;Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1997

A;Reference number: Z17305

A;Accession: T11657

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-205 <BAR>

A;Cross-references: EMBL:Z98533

C;Genetics:

A;Map position: 1L  
A;Note: SPAC6F12.06  
C;Superfamily: human rho GDP dissociation inhibitor

Query Match 62.5%; Score 5; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 40 KMDAE 44

RESULT 24

T30415

host range factor 1 - Lymantria dispar nuclear polyhedrosis virus  
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 21-Jul-2000  
C;Accession: T30415  
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrmann, G.F.  
Virology 253, 17-34, 1999  
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria dispar.  
A;Reference number: Z20836; MUID:99124785; PMID:9887315  
A;Accession: T30415  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-218 <KUZ>  
A;Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70253.1; PID:g3822302  
C;Superfamily: Lymantria dispar nuclear polyhedrosis virus host range factor 1

Query Match 62.5%; Score 5; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8  
|||||  
Db 3 MDAEF 7

RESULT 25

I55963

Lyt-2.1 lymphocyte differentiation antigen - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jan-2000  
C;Accession: I55963  
R;Liaw, C.W.; Zamoyska, R.; Parnes, J.R.  
J. Immunol. 137, 1037-1043, 1986  
A;Title: Structure, sequence, and polymorphism of the Lyt-2 T cell differentiation antigen gene.  
A;Reference number: I55963; MUID:86252252; PMID:3487583  
A;Accession: I55963  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-220 <RES>  
A;Cross-references: GB:M12979; NID:g198960; PIDN:AAA39474.1; PID:g198962

C;Genetics:

A;Introns: 149/1; 184/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;46-131/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 5; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 40 KMDAE 44

#### RESULT 26

S59147

cytochrome-c oxidase (EC 1.9.3.1) chain II - land snail mitochondrion

C;Species: mitochondrion Albinaria coerulea (land snail)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2003

C;Accession: S59147

R;Hatzoglou, E.; Rodakis, G.C.; Lecanidou, R.

Genetics 140, 1353-1366, 1995

A;Title: Complete sequence and gene organization of the mitochondrial genome of the land snail Albinaria coerulea.

A;Reference number: S59143; MUID:96120351; PMID:7498775

A;Accession: S59147

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-224 <HAT>

A;Cross-references: EMBL:X83390; NID:g975668; PIDN:CAA58300.1; PID:g975673;  
GSPDB:GN00133

C;Genetics:

A;Gene: COII

A;Genome: mitochondrion

A;Genetic code: SGC4

C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein

F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>

F;27-47/Domain: transmembrane #status predicted <TM1>

F;63-85/Domain: transmembrane #status predicted <TM2>

F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted

F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

#### RESULT 27

E34284  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - sea urchin (*Paracentrotus lividus*)  
 mitochondrion  
 C;Species: mitochondrion *Paracentrotus lividus* (common urchin)  
 C;Date: 29-Jun-1990 #sequence\_revision 29-Jun-1990 #text\_change 18-Aug-2003  
 C;Accession: E34284; D26510; T01675  
 R;Cantatore, P.; Roberti, M.; Rainaldi, G.; Gadaleta, M.N.; Saccone, C.  
 J. Biol. Chem. 264, 10965-10975, 1989  
 A;Title: The complete nucleotide sequence, gene organization, and genetic code  
 of the mitochondrial genome of *Paracentrotus lividus*.  
 A;Reference number: A34284; MUID:89291831; PMID:2544576  
 A;Accession: E34284  
 A;Molecule type: DNA  
 A;Residues: 1-229 <CAN1>  
 A;Cross-references: GB:J04815; NID:g342913; PIDN:AAA68137.1; PID:g854690  
 R;Cantatore, P.; Roberti, M.; Morisco, P.; Rainaldi, G.; Gadaleta, M.N.;  
 Saccone, C.  
 Gene 53, 41-54, 1987  
 A;Title: A novel gene order in the *Paracentrotus lividus* mitochondrial genome.  
 A;Reference number: A26510; MUID:87248108; PMID:3596250  
 A;Accession: D26510  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-8, 'P', 10, 'H' <CAN2>  
 A;Cross-references: GB:M16520; NID:g342888; PIDN:AAA31991.1; PID:g342903  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Genetic code: SGC8  
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c  
 oxidase chain II homology  
 C;Keywords: copper; electron transfer; heme; membrane-associated complex;  
 mitochondrial inner membrane; mitochondrion; oxidative phosphorylation;  
 oxidoreductase; respiratory chain; transmembrane protein  
 F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

RESULT 28  
 T11796  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - sea urchin (*Arbacia lixula*)  
 mitochondrion  
 C;Species: mitochondrion *Arbacia lixula* (black urchin)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003  
 C;Accession: T11796  
 R;De Giorgi, C.; Martiradonna, A.; Lanave, C.; Saccone, C.  
 Mol. Phylogenet. Evol. 5, 323-332, 1996

A;Title: Complete sequence of the mitochondrial DNA in the sea urchin *Arbacia lixula*: Conserved features of the echinoid mitochondrial genome.  
 A;Reference number: Z17346; MUID:96292527; PMID:8728390  
 A;Accession: T11796  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-229 <DEG>  
 A;Cross-references: EMBL:X80396; NID:g1321876; PIDN:CAA56611.1  
 A;Experimental source: eggs  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Genetic code: SGC8  
 A;Note: cytochrome C oxidase subunit 4L  
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology  
 C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein  
 F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

#### RESULT 29

D58892

cytochrome-c oxidase (EC 1.9.3.1) chain II - coelacanth mitochondrion

C;Species: mitochondrion *Latimeria chalumnae* (coelacanth)

C;Date: 30-Oct-1998 #sequence\_revision 30-Oct-1998 #text\_change 18-Aug-2003

C;Accession: D58892

R;Zardoya, R.; Meyer, A.

Genetics 146, 995-1010, 1997

A;Title: The complete DNA sequence of the mitochondrial genome of a "living fossil," the coelacanth (*Latimeria chalumnae*).

A;Reference number: A58892; MUID:97358858; PMID:9215903

A;Accession: D58892

A;Status: preliminary; nucleic acid sequence not shown; translation not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-230 <ZAR>

A;Cross-references: GB:U82228; NID:g1916817; PIDN:AAC60321.1; PID:g1916821

A;Note: submitted to GenBank/EMBL/DDBJ December, 1996

C;Genetics:

A;Gene: COII

A;Map position: FOR7180-7872

A;Genome: mitochondrion

A;Genetic code: SGC1

C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; magnesium; membrane-associated complex; metalloprotein; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein  
 F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;15-35/Domain: transmembrane helix #status predicted <TR01>  
 F;60-87/Domain: transmembrane helix #status predicted <TR02>  
 F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 30

S36009

cytochrome-c oxidase (EC 1.9.3.1) chain II - common carp mitochondrion

C;Species: mitochondrion Cyprinus carpio (common carp)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2003

C;Accession: S36009; D44650

R;Chang, Y.S.; Huang, F.L.

submitted to the EMBL Data Library, July 1991

A;Description: The cDNA and primary structure of pregrowth hormones of three species of Cyprinidae: silver carp, bighead carp and grass carp.

A;Reference number: S21910

A;Accession: S36009

A;Molecule type: DNA

A;Residues: 1-230 <CHA1>

A;Cross-references: EMBL:X61010; NID:g436882; PIDN:CAA43340.1; PID:g12842

R;Chang, Y.S.; Huang, F.L.; Lo, T.B.

J. Mol. Evol. 38, 138-155, 1994

A;Title: The complete nucleotide sequence and gene organization of carp (Cyprinus carpio) mitochondrial genome.

A;Reference number: A44650; MUID:94223691; PMID:8169959

A;Accession: D44650

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-219,'F',221-230 <CHA2>

A;Cross-references: EMBL:X61010; NID:g436882

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGCl

C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; heme; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein

F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>

F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted

F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

RESULT 31

S45491

cytochrome-c oxidase (EC 1.9.3.1) chain II - European seabass mitochondrion

C;Species: mitochondrion Dicentrarchus labrax (European seabass)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2003

C;Accession: S45491

R;Venanzetti, F.; Cecconi, F.; Giorgi, M.; Cesaroni, D.; Sbordoni, V.;

Mariottini, P.

Curr. Genet. 26, 139-145, 1994

A;Title: Cloning and characterization of the European seabass, Dicentrarchus labrax, mitochondrial genome.

A;Reference number: S45489; MUID:95094310; PMID:8001168

A;Accession: S45491

A;Molecule type: DNA

A;Residues: 1-230 <VEN>

A;Cross-references: EMBL:X74149; NID:g521078; PIDN:CAA52246.1; PID:g521079

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGCl

C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; heme; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein

F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>

F;15-35/Domain: transmembrane helix #status predicted <TR01>

F;60-87/Domain: transmembrane helix #status predicted <TR02>

F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted

F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

RESULT 32

T09860

cytochrome-c oxidase (EC 1.9.3.1) chain II - rainbow trout mitochondrion (fragment)

C;Species: mitochondrion Oncorhynchus mykiss (rainbow trout)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003

C;Accession: T09860



R;Zardoya, R.; Garrido-Pertierra, A.; Bautista, J.M.  
 J. Mol. Evol. 41, 942-951, 1995  
 A;Title: The complete nucleotide sequence of the mitochondrial DNA genome of the rainbow trout, *Oncorhynchus mykiss*.  
 A;Reference number: Z16890; MUID:96139027; PMID:8587139  
 A;Accession: T09860  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-230 <ZAR>  
 A;Cross-references: EMBL:L29771; NID:g1246865; PIDN:AAB03350.1; PID:g463157  
 C;Genetics:  
 A;Gene: COII  
 A;Genome: mitochondrion  
 A;Genetic code: SGC1  
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology  
 C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein  
 F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 33

T09950  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - Atlantic salmon mitochondrion  
 C;Species: mitochondrion *Salmo salar* (Atlantic salmon)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003  
 C;Accession: T09950  
 R;Hurst, C.D.; Bartlett, S.E.; Bruce, I.J.; Davidson, W.S.  
 submitted to the EMBL Data Library, October 1998  
 A;Description: The complete nucleotide sequence of the mitochondrial DNA of the Atlantic salmon, *Salmo salar*.  
 A;Reference number: Z16904  
 A;Accession: T09950  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-230 <HUR>  
 A;Cross-references: EMBL:U12143; NID:g3775976; PID:g3776538  
 A;Experimental source: liver  
 C;Genetics:  
 A;Gene: COII  
 A;Genome: mitochondrion  
 A;Genetic code: SGC1  
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; membrane-associated complex;  
mitochondrial inner membrane; mitochondrion; oxidative phosphorylation;  
oxidoreductase; respiratory chain; transmembrane protein  
F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

#### RESULT 34

T11290

cytochrome-c oxidase (EC 1.9.3.1) chain II - Raja radiata mitochondrion

C;Species: mitochondrion Raja radiata

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003

C;Accession: T11290

R;Rasmussen, A.S.; Arnason, U.

Proc. Natl. Acad. Sci. U.S.A. 96, 2177-2182, 1999

A;Title: Molecular studies suggest that cartilaginous fishes have an apical position in the piscine tree.

A;Reference number: Z17259; MUID:99162577; PMID:10051614

A;Accession: T11290

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-230 <RAS>

A;Cross-references: EMBL:AF106038; NID:g4406269; PID:g4406273; PIDN:AAD19932.1

C;Genetics:

A;Gene: COX-II

A;Genome: mitochondrion

A;Genetic code: SGCl

C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; membrane-associated complex;  
mitochondrial inner membrane; mitochondrion; oxidative phosphorylation;  
oxidoreductase; respiratory chain; transmembrane protein

F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>

F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted

F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

#### RESULT 35

T11303  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - smaller spotted catshark  
 mitochondrion (fragment)  
 C;Species: mitochondrion Scyliorhinus canicula (smaller spotted catshark,  
 smaller spotted dogfish)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003  
 C;Accession: T11303  
 R;Delarbre, C.; Spruyt, N.; Delmarre, C.; Gallut, C.; Barriel, V.; Janvier, P.;  
 Laudet, V.; Gachelin, G.  
 Genetics 150, 331-344, 1998  
 A;Title: The complete nucleotide sequence of the mitochondrial DNA of the  
 Dogfish, Scyliorhinus canicula.  
 A;Reference number: Z17260; MUID:98393590; PMID:9725850  
 A;Accession: T11303  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-230 <DEL>  
 A;Cross-references: EMBL:Y16067; NID:g3618230; PIDN:CAA76022.1; PID:g3618234  
 A;Experimental source: muscle  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Genetic code: SGC1  
 A;Note: CO II  
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c  
 oxidase chain II homology  
 C;Keywords: copper; electron transfer; membrane-associated complex;  
 mitochondrial inner membrane; mitochondrion; oxidative phosphorylation;  
 oxidoreductase; respiratory chain; transmembrane protein  
 F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 36

T11537  
 cytochrome-c oxidase (EC 1.9.3.1) chain II - spiny dogfish mitochondrion  
 (fragment)  
 C;Species: mitochondrion Squalus acanthias (spiny dogfish)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003  
 C;Accession: T11537  
 R;Rasmussen, A.S.; Arnason, U.  
 J. Mol. Evol. 48, 118-123, 1999  
 A;Title: Phylogenetic studies of complete mitochondrial DNA molecules place  
 cartilaginous fishes within the tree of bony fishes.  
 A;Reference number: Z17281; MUID:99091711; PMID:9873084  
 A;Accession: T11537  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-230 <RAS>

A;Cross-references: EMBL:Y18134; NID:g4186095; PIDN:CAA77052.1; PID:g4186099  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Genetic code: SGC1  
 C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology  
 C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein  
 F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
 F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
 F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
 F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 37

T11767

cytochrome-c oxidase (EC 1.9.3.1) chain II - Mustelus manazo mitochondrion (fragment)

C;Species: mitochondrion Mustelus manazo

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 18-Aug-2003

C;Accession: T11767

R;Cao, Y.; Waddell, P.J.; Okada, N.; Hasegawa, M.

Mol. Biol. Evol. 15, 1637-1646, 1998

A;Title: The complete mitochondrial DNA sequence of the shark (Mustelus manazo): Evaluating rooting contradictions to living bony vertebrates.

A;Reference number: Z17338; MUID:99083431; PMID:9866199

A;Accession: T11767

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-230 <CAO>

A;Cross-references: EMBL:AB015962; PIDN:BAA33055.1

A;Experimental source: liver

C;Genetics:

A;Genome: mitochondrion

A;Note: COII

C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology

C;Keywords: copper; electron transfer; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein

F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>

F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted

F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match 62.5%; Score 5; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            2 VKMDA 6  
             |||||  
Db           170 VKMDA 174

RESULT 38

E84673

hypothetical protein At2g27490 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C;Accession: E84673

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;  
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,  
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,  
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,  
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,  
G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,  
C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84673

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-232 <STO>

A;Cross-references: GB:AE002093; NID:g4314391; PIDN:AAD15601.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g27490

A;Map position: 2

Query Match	62.5%;	Score 5;	DB 2;	Length 232;
Best Local Similarity	100.0%;	Pred. No. 81;		
Matches	5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy            1 EVKMD 5  
             |||||  
Db           119 EVKMD 123

RESULT 39

S35465

cytochrome-c oxidase (EC 1.9.3.1) chain II - hillstream loach (Crossostoma  
lacustre) mitochondrion

C;Species: mitochondrion Crossostoma lacustre

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Aug-2003

C;Accession: S35465; S60274

R;Tzeng, C.S.; Hui, C.F.; Shen, S.C.; Huang, P.C.

Nucleic Acids Res. 20, 4853-4858, 1992

A;Title: The complete nucleotide sequence of the Crossostoma lacustre  
mitochondrial genome: conservation and variations among vertebrates.

A;Reference number: S35462; MUID:93027205; PMID:1408800

A;Accession: S35465

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-234 <TZE1>

A;Cross-references: EMBL:M91245  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992  
R;Tzeng, C.S.; Shen, S.C.; Huang, P.C.  
Bull. Inst. Zool. Acad. Sin. 29, 11-19, 1990  
A;Title: Mitochondrial DNA identity of Crossostoma (Homalopteridae, Pisces) from two river systems of the same geographical origin.  
A;Reference number: S60271  
A;Accession: S60274  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-230 <TZE2>  
A;Cross-references: GB:M91245; NID:g1381122; PIDN:AAB96814.1; PID:g336707  
C;Genetics:  
A;Genome: mitochondrion  
A;Genetic code: SGC1  
C;Superfamily: cytochrome-c oxidase chain II, mitochondrial type; cytochrome-c oxidase chain II homology  
C;Keywords: copper; electron transfer; heme; membrane-associated complex; mitochondrial inner membrane; mitochondrion; oxidative phosphorylation; oxidoreductase; respiratory chain; transmembrane protein  
F;9-214/Domain: cytochrome-c oxidase chain II homology <CO2>  
F;161,196,200,207/Binding site: copper 1 (His, Cys, Cys, Met) #status predicted  
F;196,198,200,204/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted  
F;198/Binding site: magnesium (Glu) (shared with chain I) #status predicted

Query Match	62.5%;	Score 5;	DB 2;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 81;		
Matches	5;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy            2 VKMDA 6  
              | | | | |  
Db            170 VKMDA 174

#### RESULT 40

A29523  
T-cell surface glycoprotein Lyt-2 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 21-Jul-2000  
C;Accession: A29523  
R;Nakauchi, H.; Tagawa, M.; Nolan, G.P.; Herzenberg, L.A.  
Nucleic Acids Res. 15, 4337-4347, 1987  
A;Title: Isolation and characterization of the gene for the murine T cell differentiation antigen and immunoglobulin-related molecule, Lyt-2.  
A;Reference number: A29523; MUID:87231009; PMID:3495785  
A;Accession: A29523  
A;Molecule type: DNA  
A;Residues: 1-246 <NAK>  
A;Cross-references: GB:Y00157; NID:g52967; PIDN:CAA68352.2; PID:g4688926  
C;Genetics:  
A;Introns: 148/1; 183/1; 220/1; 230/2  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein; transmembrane protein  
F;46-130/Domain: immunoglobulin homology <IMM>

Query Match	62.5%;	Score 5;	DB 2;	Length 246;
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Best Local Similarity 100.0%; Pred. No. 85;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 40 KMDAE 44

Search completed: March 26, 2004, 15:35:42  
Job time : 49.5 secs



OM protein - protein search, using sw model

Run on: March 26, 2004, 15:35:53 ; Search time 35.5 Seconds  
(without alignments)  
58.966 Million cell updates/sec

Title: US-09-668-314C-70  
Perfect score: 8  
Sequence: 1 EVKMDAEF 8

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1065169 seqs, 261661801 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1065169

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							

1	8	100.0	8	9	US-09-794-927-67	Sequence 67, Appl
2	8	100.0	8	9	US-09-795-847-67	Sequence 67, Appl
3	8	100.0	8	9	US-09-794-743-67	Sequence 67, Appl
4	8	100.0	8	9	US-09-794-748-67	Sequence 67, Appl
5	8	100.0	8	9	US-09-794-925-67	Sequence 67, Appl
6	8	100.0	8	9	US-09-681-442-67	Sequence 67, Appl
7	8	100.0	8	10	US-09-869-414-67	Sequence 67, Appl
8	8	100.0	8	12	US-10-652-927-67	Sequence 67, Appl
9	8	100.0	8	12	US-10-652-830-67	Sequence 67, Appl
10	8	100.0	8	15	US-10-427-208-52	Sequence 52, Appl
11	8	100.0	9	13	US-10-016-717-6	Sequence 6, Appli
12	8	100.0	9	14	US-10-066-319-3	Sequence 3, Appli
13	8	100.0	10	9	US-09-794-927-64	Sequence 64, Appl
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249	5	62.5	2120	14	US-10-320-175-3	Sequence 3, Appli
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252	4	50.0	4	13	US-10-016-717-2	Sequence 2, Appli
253	4	50.0	4	14	US-10-100-957A-92	Sequence 92, Appl
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259	4	50.0	5	9	US-09-794-925-72	Sequence 72, Appl
260	4	50.0	5	9	US-09-681-442-72	Sequence 72, Appl
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263	4	50.0	5	12	US-10-652-830-72	Sequence 72, Appl
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#### ALIGNMENTS

##### RESULT 1

US-09-794-927-67

; Sequence 67, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/794,927

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-794-927-67

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Best Local Similarity 100.0%; Pred. No. 9.6e+05;
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# RESULT 2

US-09-795-847-67

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; Sequence 67, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
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; TYPE: PRT  
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US-09-795-847-67

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Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
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; Patent No. US20010021391A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280BC  
; CURRENT APPLICATION NUMBER: US/09/794,743  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
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; PRIOR APPLICATION NUMBER: 09/404,133  
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US-09-794-743-67

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RESULT 4

US-09-794-748-67

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; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND  
; TITLE OF INVENTION: USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280JL  
; CURRENT APPLICATION NUMBER: US/09/794,748  
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US-09-794-748-67

Query Match                    100.0%; Score 8; DB 9; Length 8;  
Best Local Similarity        100.0%; Pred. No. 9.6e+05;  
Matches        8; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy                    1 EVKMDAEF 8  
                      |||||  
Db                    1 EVKMDAEF 8

RESULT 5

US-09-794-925-67

; Sequence 67, Application US/09794925  
; Patent No. US20020064819A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.

```

; APPLICANT:  Heinrikson, Robert L.
; APPLICANT:  Parodi, Luis A.
; APPLICANT:  Yan, Riqiang
; TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION:  THEREFOR
; FILE REFERENCE:  28341/6280HI
; CURRENT APPLICATION NUMBER:  US/09/794,925
; CURRENT FILING DATE:  2001-02-27
; PRIOR APPLICATION NUMBER:  09/416,901
; PRIOR FILING DATE:  1999-10-13
; PRIOR APPLICATION NUMBER:  60/155,493
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  09/404,133
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  PCT/US99/20881
; PRIOR FILING DATE:  1999-09-23
; PRIOR APPLICATION NUMBER:  60/101,594
; PRIOR FILING DATE:  1998-09-24
; NUMBER OF SEQ ID NOS:  73
; SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH:  8
; TYPE:  PRT
; ORGANISM:  Artificial Sequence
; FEATURE:
; OTHER INFORMATION:  Description of Artificial Sequence:  Peptide
US-09-794-925-67

```

```

Query Match          100.0%;  Score 8;  DB 9;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 9.6e+05;
Matches      8;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

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Qy          1 EVKMDAEF 8
             |||||
Db          1 EVKMDAEF 8

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# RESULT 6

US-09-681-442-67

```

; Sequence 67, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT:  Gurney, Mark E.
; APPLICANT:  Bienkowski, Michael J.
; APPLICANT:  Heinrikson, Robert L.
; APPLICANT:  Parodi, Luis A.
; APPLICANT:  Yan, Riqiang
; TITLE OF INVENTION:  ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND USES
; TITLE OF INVENTION:  THEREFOR
; FILE REFERENCE:  28341/6280FG
; CURRENT APPLICATION NUMBER:  US/09/681,442
; CURRENT FILING DATE:  2001-04-05
; PRIOR APPLICATION NUMBER:  09/416,901
; PRIOR FILING DATE:  1999-10-13
; PRIOR APPLICATION NUMBER:  60/155,493

```

; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 67  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
US-09-681-442-67

Query Match 100.0%; Score 8; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 1 EVKMDAEF 8

RESULT 7

US-09-869-414-67

; Sequence 67, Application US/09869414  
; Publication No. US20030077226A1  
; GENERAL INFORMATION:  
; APPLICANT: Beinkowski et al.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280M  
; CURRENT APPLICATION NUMBER: US/09/869,414  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 67  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide  
US-09-869-414-67

Query Match 100.0%; Score 8; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 1 EVKMDAEF 8

RESULT 8

US-10-652-927-67

; Sequence 67, Application US/10652927

; Publication No. US20040043408A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor  
and Uses

; TITLE OF INVENTION: Therefor

; FILE REFERENCE: 29915/6280N3

; CURRENT APPLICATION NUMBER: US/10/652,927

; CURRENT FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 09/794,925

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 67

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-10-652-927-67

Query Match 100.0%; Score 8; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 1 EVKMDAEF 8

RESULT 9

US-10-652-830-67

; Sequence 67, Application US/10652830

; Publication No. US20040048303A1

```

; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-652-830-67

```

```

Query Match          100.0%; Score 8; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      1 EVKMDAEF 8

```

# RESULT 10

US-10-427-208-52

; Sequence 52, Application US/10427208

; Publication No. US20030200555A1

## ; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Hazuda, Daria J

; APPLICANT: Chen Dodson, Elizabeth

; APPLICANT: Lai, Ming-Tain

; APPLICANT: Xu, Min

; APPLICANT: Shi, Xiao-Ping

; APPLICANT: Simon, Adam J.

; APPLICANT: Wu, Guoxin

; APPLICANT: Li, Yueming

; APPLICANT: Register, Robert B.

; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED

; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE  
ACTIVITY

; FILE REFERENCE: 21052  
; CURRENT APPLICATION NUMBER: US/10/427,208  
; CURRENT FILING DATE: 2003-04-30  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 52  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-427-208-52

Query Match 100.0%; Score 8; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 1 EVKMDAEF 8

RESULT 11

US-10-016-717-6

; Sequence 6, Application US/10016717  
; Publication No. US20020132281A1  
; GENERAL INFORMATION:  
; APPLICANT: Hook, Vivian Y.H.  
; TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA  
; FILE REFERENCE: P-AS 5031  
; CURRENT APPLICATION NUMBER: US/10/016,717  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: US 09/173,887  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 09/294,987  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: mammalian  
US-10-016-717-6

Query Match 100.0%; Score 8; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 12

US-10-066-319-3

; Sequence 3, Application US/10066319  
; Publication No. US20030147810A1  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Brian D.

; APPLICANT: Rehemtulla, Alnawaz  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REPORTING  
; TITLE OF INVENTION: OF PROTEASE ACTIVITY WITHIN THE SECRETORY PATHWAY  
; FILE REFERENCE: 11203-007001  
; CURRENT APPLICATION NUMBER: US/10/066,319  
; CURRENT FILING DATE: 2002-06-17  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-066-319-3

Query Match 100.0%; Score 8; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 13

US-09-794-927-64

; Sequence 64, Application US/09794927  
; Patent No. US20010016324A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND  
; TITLE OF INVENTION: USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280FG  
; CURRENT APPLICATION NUMBER: US/09/794,927  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:



; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-794-927-64

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 14

US-09-795-847-64

; Sequence 64, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-795-847-64

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 15

US-09-794-743-64

; Sequence 64, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-794-743-64

Query Match 100.0%; Score 8; DB 9; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0068;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 2 EVKMDAEF 9

RESULT 16

US-09-794-748-64

; Sequence 64, Application US/09794748

; Patent No. US20020037315A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND  
; TITLE OF INVENTION: USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280JL  
; CURRENT APPLICATION NUMBER: US/09/794,748  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-794-748-64

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

# RESULT 17

US-09-796-264-4

; Sequence 4, Application US/09796264  
; Patent No. US20020049303A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Jordan J.N.  
; APPLICANT: Lin, Xinli  
; APPLICANT: Koelsch, Gerald  
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods  
; TITLE OF INVENTION: of Use Thereof  
; FILE REFERENCE: OMRF 179  
; CURRENT APPLICATION NUMBER: US/09/796,264  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 09/604,608  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: 60/168,060  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: 60/177,836  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 60/178,368  
; PRIOR FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: 60/210,292  
; PRIOR FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-796-264-4

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 18

US-09-794-925-64

; Sequence 64, Application US/09794925  
; Patent No. US20020064819A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Bienkowski, Michael J.  
; APPLICANT: Heinrikson, Robert L.  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Yan, Riqiang  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280HI  
; CURRENT APPLICATION NUMBER: US/09/794,925  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-794-925-64

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | |  
Db 2 EVKMDAEF 9

RESULT 19

US-09-681-442-64

; Sequence 64, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-681-442-64

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | |  
Db 2 EVKMDAEF 9

RESULT 20

US-09-845-226-4

; Sequence 4, Application US/09845226

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; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRF 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-845-226-4

```

```

Query Match          100.0%; Score 8; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      2 EVKMDAEF 9

```

# RESULT 21

US-09-795-903A-4

```

; Sequence 4, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; TITLE OF INVENTION: of Use Thereof
; FILE REFERENCE: OMRF 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25

```

; PRIOR APPLICATION NUMBER: 60/178,368  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: 60/210,292  
; PRIOR FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-795-903A-4

Query Match 100.0%; Score 8; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 22

US-09-869-414-64

; Sequence 64, Application US/09869414  
; Publication No. US20030077226A1  
; GENERAL INFORMATION:  
; APPLICANT: Beinkowski et al.  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 28341/6280M  
; CURRENT APPLICATION NUMBER: US/09/869,414  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 09/416,901  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: 60/155,493  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 09/404,133  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-869-414-64

Query Match 100.0%; Score 8; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;



Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
      |||||||  
Db 2 EVKMDAEF 9

RESULT 23

US-09-548-366-64

; Sequence 64, Application US/09548366

; Publication No. US20030104365A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,  
AND

; TITLE OF INVENTION: USES THEREFOR

; FILE REFERENCE: 28341/6280A

; CURRENT APPLICATION NUMBER: US/09/548,366

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-548-366-64

Query Match 100.0%; Score 8; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0068;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
      |||||||  
Db 2 EVKMDAEF 9

RESULT 24

US-10-652-927-64

; Sequence 64, Application US/10652927

; Publication No. US20040043408A1

; GENERAL INFORMATION:

; APPLICANT: Gurney et al.

```

; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N3
; CURRENT APPLICATION NUMBER: US/10/652,927
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-652-927-64

```

```

Query Match          100.0%; Score 8; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 EVKMDAEF 8
        |||||
Db      2 EVKMDAEF 9

```

# RESULT 25

US-10-652-830-64

```

; Sequence 64, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor
and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23

```

; PRIOR APPLICATION NUMBER: PCT/US99/20881  
; PRIOR FILING DATE: 1999-09-23  
; PRIOR APPLICATION NUMBER: 60/101,594  
; PRIOR FILING DATE: 1998-09-24  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-652-830-64

Query Match 100.0%; Score 8; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 26

US-10-032-818-7

; Sequence 7, Application US/10032818  
; Publication No. US20030092629A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Jordan J.N.  
; APPLICANT: Koelsch, Gerald  
; APPLICANT: Ghosh, Arun K.  
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof  
; FILE REFERENCE: 2932.1006-007  
; CURRENT APPLICATION NUMBER: US/10/032,818  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 60/275,756  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: US 60/258,705  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-032-818-7

Query Match 100.0%; Score 8; DB 14; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0068;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 27

US-10-427-208-53

; Sequence 53, Application US/10427208

; Publication No. US20030200555A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Hazuda, Daria J

; APPLICANT: Chen Dodson, Elizabeth

; APPLICANT: Lai, Ming-Tain

; APPLICANT: Xu, Min

; APPLICANT: Shi, Xiao-Ping

; APPLICANT: Simon, Adam J.

; APPLICANT: Wu, Guoxin

; APPLICANT: Li, Yueming

; APPLICANT: Register, Robert B.

; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED

; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE  
ACTIVITY

; FILE REFERENCE: 21052

; CURRENT APPLICATION NUMBER: US/10/427,208

; CURRENT FILING DATE: 2003-04-30

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 53

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-427-208-53

Query Match 100.0%; Score 8; DB 15; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0068;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8

|||||||

Db 2 EVKMDAEF 9

RESULT 28

US-10-354-955-1

; Sequence 1, Application US/10354955

; Publication No. US20030171291A1

; GENERAL INFORMATION:

; APPLICANT: Gary Christie

; APPLICANT: Ishrut Hussain

; APPLICANT: David J. Powell

; TITLE OF INVENTION: No. US20030171291A1el Treatment

; FILE REFERENCE: P32448

; CURRENT APPLICATION NUMBER: US/10/354,955

; CURRENT FILING DATE: 2003-01-30

; PRIOR APPLICATION NUMBER: 09/693,744

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 9925136.5

; PRIOR FILING DATE: 1999-10-22

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-10-354-955-1

Query Match 100.0%; Score 8; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 3 EVKMDAEF 10

RESULT 29

US-10-354-955-3

; Sequence 3, Application US/10354955  
; Publication No. US20030171291A1  
; GENERAL INFORMATION:  
; APPLICANT: Gary Christie  
; APPLICANT: Ishrut Hussain  
; APPLICANT: David J. Powell  
; TITLE OF INVENTION: No. US20030171291A1el Treatment  
; FILE REFERENCE: P32448  
; CURRENT APPLICATION NUMBER: US/10/354,955  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: 09/693,744  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 9925136.5  
; PRIOR FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion protein with maltose binding protein attached at  
residue 1'  
US-10-354-955-3

Query Match 100.0%; Score 8; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 3 EVKMDAEF 10

RESULT 30

US-09-896-874-2

; Sequence 2, Application US/09896874  
; Patent No. US20020016320A1  
; GENERAL INFORMATION:  
; APPLICANT: Fang, Lawrence Y.

```
; APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.40USU1
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-896-874-2
```

```
Query Match          100.0%; Score 8; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches      8; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy          1 EVKMDAEF 8
             |||||
Db          2 EVKMDAEF 9
```

RESULT 31

US-09-896-139-2

```
; Sequence 2, Application US/09896139
; Patent No. US20020128255A1
; GENERAL INFORMATION:
; APPLICANT: Beck, James P.
; APPLICANT: Fang, Lawrence Y.
; APPLICANT: Freskos, John N.
; APPLICANT: Gailunas, Andrea
; APPLICANT: Hom, Roy
; APPLICANT: Jagodzinska, Barbara
; APPLICANT: John, Varghese
; APPLICANT: Maillaird, Michel
; APPLICANT: Pulley, Shon R.
; APPLICANT: TenBrink, Ruth E.
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; FILE REFERENCE: 13615.25USU4
; CURRENT APPLICATION NUMBER: US/09/896,139
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,323
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/252,736
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/255,956
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/268,497
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: US 60/279,779
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: US 60/295,589
; PRIOR FILING DATE: 2001-06-04
```

; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-896-139-2

Query Match 100.0%; Score 8; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

RESULT 32

US-09-895-843-2

; Sequence 2, Application US/09895843  
; Patent No. US20020143177A1  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James P.  
; APPLICANT: Fang, Lawrence Y.  
; APPLICANT: Freskos, John N.  
; APPLICANT: Gailunas, Andrea  
; APPLICANT: Hom, Roy  
; APPLICANT: Jagodzinska, Barbara  
; APPLICANT: John, Varghese  
; APPLICANT: Maillaird, Michel  
; APPLICANT: Pulley, Shon R.  
; APPLICANT: TenBrink, Ruth E.  
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE  
; FILE REFERENCE: 13615.41USU1  
; CURRENT APPLICATION NUMBER: US/09/895,843  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/215,323  
; PRIOR FILING DATE: 2000-06-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-895-843-2

Query Match 100.0%; Score 8; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9



RESULT 33

US-09-895-871-2

; Sequence 2, Application US/09895871  
 ; Publication No. US20030096864A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fang, Lawrence Y.  
 ; APPLICANT: Hom, Roy  
 ; APPLICANT: John, Varghese  
 ; APPLICANT: Maillaird, Michel  
 ; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE  
 ; FILE REFERENCE: 13615.21USU1  
 ; CURRENT APPLICATION NUMBER: US/09/895,871  
 ; CURRENT FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/215,323  
 ; PRIOR FILING DATE: 2000-06-30  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-09-895-871-2

Query Match 100.0%; Score 8; DB 10; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.0079;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

RESULT 34

US-10-427-208-54

; Sequence 54, Application US/10427208  
 ; Publication No. US20030200555A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Hazuda, Daria J  
 ; APPLICANT: Chen Dodson, Elizabeth  
 ; APPLICANT: Lai, Ming-Tain  
 ; APPLICANT: Xu, Min  
 ; APPLICANT: Shi, Xiao-Ping  
 ; APPLICANT: Simon, Adam J.  
 ; APPLICANT: Wu, Guoxin  
 ; APPLICANT: Li, Yueming  
 ; APPLICANT: Register, Robert B.  
 ; TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED  
 ; TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE  
 ACTIVITY  
 ; FILE REFERENCE: 21052  
 ; CURRENT APPLICATION NUMBER: US/10/427,208  
 ; CURRENT FILING DATE: 2003-04-30

; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 54  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-427-208-54

Query Match 100.0%; Score 8; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0079;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 3 EVKMDAEF 10

RESULT 35

US-10-299-739-2

; Sequence 2, Application US/10299739  
; Publication No. US20040039064A1  
; GENERAL INFORMATION:  
; APPLICANT: Elan Pharmaceuticals, Inc.  
; APPLICANT: Pharmacia & Upjohn Company  
; APPLICANT: Romero, Arthur G.  
; APPLICANT: Schostarez, Heinrich J.  
; APPLICANT: Christina, McGrain M.  
; TITLE OF INVENTION: Amine 1,2- and 1,3-Diol Compounds  
; FILE REFERENCE: 01-1724-B  
; CURRENT APPLICATION NUMBER: US/10/299,739  
; CURRENT FILING DATE: 2003-11-19  
; PRIOR APPLICATION NUMBER: 60/333,081  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/334,000  
; PRIOR FILING DATE: 2001-11-18  
; PRIOR APPLICATION NUMBER: 60/362,752  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: N-terminal biotin  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (11)..(11)  
; OTHER INFORMATION: covalent attachment of oregon green  
US-10-299-739-2

Query Match 100.0%; Score 8; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0085;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 2 EVKMDAEF 9

RESULT 36

US-10-084-380A-7

; Sequence 7, Application US/10084380A  
; Publication No. US20030073655A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset Biopharmaceutical Inc.  
; APPLICANT: Chain, Daniel G.  
; TITLE OF INVENTION: specific antibodies to amyloid beta peptide,  
pharmaceutical compositions  
; TITLE OF INVENTION: and methods of use thereof  
; FILE REFERENCE: P-4815-US1  
; CURRENT APPLICATION NUMBER: US/10/084,380A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 60/041,850  
; PRIOR FILING DATE: 1997-04-09  
; PRIOR APPLICATION NUMBER: 09/402,820  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: pct/us98/06900  
; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: human  
US-10-084-380A-7

Query Match 100.0%; Score 8; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 4 EVKMDAEF 11

RESULT 37

US-10-192-625-2

; Sequence 2, Application US/10192625  
; Publication No. US20030083353A1  
; GENERAL INFORMATION:  
; APPLICANT: Schostarez, Heinrich J.  
; APPLICANT: Chrusciel, Robert A  
; TITLE OF INVENTION: Diaminediols for the Treatment of Alzheimer's Disease  
; FILE REFERENCE: 01-1645-B  
; CURRENT APPLICATION NUMBER: US/10/192,625  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: 60/304,305  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/334,480

```

; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: covalent attachment of oregon green
US-10-192-625-2

```

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Query Match          100.0%; Score 8; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

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Qy          1 EVKMDAEF 8
             |||||
Db          2 EVKMDAEF 9

```

# RESULT 38

US-10-192-424-2

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; Sequence 2, Application US/10192424
; Publication No. US20030083356A1
; GENERAL INFORMATION:
; APPLICANT: Schostarez, Heinrich J.
; APPLICANT: Chrusciel, Robert A.
; TITLE OF INVENTION: Statine Derivatives for the Treatment of Alzheimer's
Disease
; FILE REFERENCE: 02-154-A
; CURRENT APPLICATION NUMBER: US/10/192,424
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/204,128
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/327,424
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal biotin
; FEATURE:

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; NAME/KEY: MISC\_FEATURE  
; LOCATION: (11)..(11)  
; OTHER INFORMATION: covalent attachment of oregon green  
US-10-192-424-2

Query Match 100.0%; Score 8; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 39

US-10-183-126A-2

; Sequence 2, Application US/10183126A

; Publication No. US20030083518A1

; GENERAL INFORMATION:

; APPLICANT: Pharmacia and Upjohn Company

; APPLICANT: John, Varghese

; APPLICANT: Hom, Roy

; APPLICANT: Tucker, John

; TITLE OF INVENTION: Substituted Alcohols Useful in Treatment of Alzheimer's Disease

; FILE REFERENCE: 01-1704-C

; CURRENT APPLICATION NUMBER: US/10/183,126A

; CURRENT FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: A synthetic APP substrate that can be cleaved by beta-secretase.

; FEATURE:

; NAME/KEY: MISC\_FEATURE

; LOCATION: (1)..(1)

; OTHER INFORMATION: N-terminal biotin

; FEATURE:

; NAME/KEY: MISC\_FEATURE

; LOCATION: (11)..(11)

; OTHER INFORMATION: Covalent attachment of Oregon green.

US-10-183-126A-2

Query Match 100.0%; Score 8; DB 14; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0085;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||  
Db 2 EVKMDAEF 9

RESULT 40

US-10-171-343-2  
 ; Sequence 2, Application US/10171343  
 ; Publication No. US20030092747A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schostarez, Heinrich J.  
 ; APPLICANT: Chrusciel, Rober A.  
 ; TITLE OF INVENTION: Aminediols for the Treatment of Alzheimer's Disease  
 ; FILE REFERENCE: 01-1644-B  
 ; CURRENT APPLICATION NUMBER: US/10/171,343  
 ; CURRENT FILING DATE: 2002-06-13  
 ; PRIOR APPLICATION NUMBER: US 60/297,827  
 ; PRIOR FILING DATE: 2001-06-13  
 ; PRIOR APPLICATION NUMBER: US 60/333,084  
 ; PRIOR FILING DATE: 2001-11-19  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic peptide  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (1)..(1)  
 ; OTHER INFORMATION: N-terminal biotin  
 ; FEATURE:  
 ; NAME/KEY: MISC\_FEATURE  
 ; LOCATION: (11)..(11)  
 ; OTHER INFORMATION: covalent attachment of oregon green  
 US-10-171-343-2

Query Match 100.0%; Score 8; DB 14; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.0085;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

Search completed: March 26, 2004, 15:44:03  
 Job time : 46.5 secs

OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:32 ; Search time 36 Seconds  
(without alignments)  
70.115 Million cell updates/sec

Title: US-09-668-314C-70  
Perfect score: 8  
Sequence: 1 EVKMDAEF 8

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result	Query					
No.	Score	Match	Length	DB	ID	Description
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1	8	100.0	35	4	Q8WZ99	Q8wz99 homo sapien
2	8	100.0	79	11	O35463	O35463 cricetulus
3	8	100.0	82	4	Q16020	Q16020 homo sapien
4	8	100.0	82	4	Q16014	Q16014 homo sapien
5	8	100.0	82	4	Q16019	Q16019 homo sapien
6	8	100.0	113	13	Q8JH58	Q8jh58 chelydra se
7	8	100.0	218	11	Q8BPV5	Q8bpv5 mus musculu
8	8	100.0	384	11	Q8BPC7	Q8bpc7 mus musculu
9	8	100.0	534	13	O93296	O93296 gallus gall
10	8	100.0	569	13	Q9PVL1	Q9pvl1 gallus gall
11	8	100.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
12	8	100.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
13	7	87.5	2148	5	Q8IPL5	Q8ipl5 drosophila
14	6	75.0	254	5	Q8IK90	Q8ik90 plasmodium
15	6	75.0	430	16	Q8A7J6	Q8a7j6 bacteroides
16	6	75.0	482	3	Q8NIL0	Q8nil0 cryptococcu
17	6	75.0	637	16	Q7WP80	Q7wp80 bordetella
18	6	75.0	637	16	Q7W1H0	Q7wlh0 bordetella
19	6	75.0	1080	16	Q898I7	Q898i7 clostridium
20	5	62.5	84	12	Q80LR6	Q80lr6 adoxophyes
21	5	62.5	98	16	Q9X9L6	Q9x9l6 salmonella
22	5	62.5	104	16	Q8RFK9	Q8rfk9 fusobacteri
23	5	62.5	127	17	Q97XY5	Q97xy5 sulfolobus
24	5	62.5	140	5	O45467	O45467 caenorhabdi
25	5	62.5	146	17	O26386	O26386 methanobact
26	5	62.5	147	5	Q8SU54	Q8su54 encephalito
27	5	62.5	149	10	Q9AU03	Q9au03 chlamydomon
28	5	62.5	150	13	Q9PSV2	Q9psv2 anguilla ja
29	5	62.5	153	10	Q9AYR9	Q9ayr9 chlamydomon
30	5	62.5	153	10	Q9AU02	Q9au02 chlamydomon
31	5	62.5	153	16	Q92VL2	Q92vl2 rhizobium m
32	5	62.5	155	10	Q8H004	Q8h004 oryza sativ
33	5	62.5	155	16	Q896C5	Q896c5 clostridium
34	5	62.5	163	17	Q8TX53	Q8tx53 methanopyru
35	5	62.5	174	8	Q9B2F3	Q9b2f3 beroe ovata
36	5	62.5	175	2	Q847P4	Q847p4 aster yello
37	5	62.5	179	16	Q97NQ1	Q97nq1 streptococc
38	5	62.5	179	16	Q8DNE5	Q8dne5 streptococc
39	5	62.5	184	8	Q9B2F6	Q9b2f6 halichondri
40	5	62.5	185	16	Q82W02	Q82w02 nitrosomona
41	5	62.5	194	8	Q8LZR7	Q8lzt7 copris luna
42	5	62.5	194	8	Q8LZR5	Q8lzt5 copris hisp
43	5	62.5	194	8	Q8LZR3	Q8lzt3 sisypus sc
44	5	62.5	194	13	Q801G5	Q80lg5 petromyzon
45	5	62.5	195	8	Q8M1C5	Q8mlc5 brugia timo
46	5	62.5	205	3	O14224	O14224 schizosacch
47	5	62.5	206	16	Q8VUW0	Q8vuwo staphylococ
48	5	62.5	216	5	Q9NHN9	Q9nhn9 drosophila
49	5	62.5	216	5	Q9VZ23	Q9vzt3 drosophila
50	5	62.5	216	16	Q8E9L6	Q8e9l6 shewanella
51	5	62.5	217	2	Q8VQG0	Q8vqg0 xenorhabdus
52	5	62.5	220	11	Q61816	Q61816 mus musculu
53	5	62.5	222	11	Q8CAX3	Q8cax3 mus musculu
54	5	62.5	222	11	Q8C2L1	Q8c2l1 mus musculu
55	5	62.5	224	8	Q8Hmw5	Q8hmw5 notacanthus
56	5	62.5	225	8	Q9MNJ2	Q9mnj2 helobdella
57	5	62.5	228	8	Q94T17	Q94t17 caelorinchu

58	5	62.5	228	8	Q9T9G2	Q9t9g2	pupa strigo
59	5	62.5	228	8	Q8HM76	Q8hm76	lophius lit
60	5	62.5	229	8	Q37394	Q37394	arbacia lix
61	5	62.5	229	8	Q8HL90	Q8hl90	synbranchus
62	5	62.5	229	8	Q8HKQ8	Q8hkq8	aspasma min
63	5	62.5	230	8	Q9ZY42	Q9zy42	raja radiat
64	5	62.5	230	8	Q95A22	Q95a22	conger myri
65	5	62.5	230	8	Q94RJ9	Q94rj9	chimaera mo
66	5	62.5	230	8	Q94SG5	Q94sg5	monopterus
67	5	62.5	230	8	Q94T04	Q94t04	mugil cepha
68	5	62.5	230	8	Q94ST2	Q94st2	danaceticht
69	5	62.5	230	8	Q94P17	Q94p17	saurida und
70	5	62.5	230	8	Q94YQ3	Q94yq3	osteoglossu
71	5	62.5	230	8	Q9B616	Q9b616	carassius a
72	5	62.5	230	8	Q9XK41	Q9xk41	salvelinus
73	5	62.5	230	8	Q94SY4	Q94sy4	cololabis s
74	5	62.5	230	8	Q94SU5	Q94su5	poromitra o
75	5	62.5	230	8	Q9XPF9	Q9xpf9	gonostoma g
76	5	62.5	230	8	Q94SJ1	Q94sj1	antigonias c
77	5	62.5	230	8	O79562	O79562	mustelus ma
78	5	62.5	230	8	Q94SP3	Q94sp3	beryx splen
79	5	62.5	230	8	Q94SN0	Q94sn0	myripristis
80	5	62.5	230	8	Q94SK4	Q94sk4	zenopsis ne
81	5	62.5	230	8	Q9B632	Q9b632	anguilla ja
82	5	62.5	230	8	Q94SR9	Q94sr9	rondeletia
83	5	62.5	230	8	Q94SB3	Q94sb3	pagrus majo
84	5	62.5	230	8	Q94TH9	Q94th9	ateleopus j
85	5	62.5	230	8	Q8WFX4	Q8wfx4	crenimugil
86	5	62.5	230	8	Q37716	Q37716	dicentrarch
87	5	62.5	230	8	Q94T39	Q94t39	polymixia l
88	5	62.5	230	8	Q94TJ2	Q94tj2	chauliodus
89	5	62.5	230	8	Q94SC6	Q94sc6	helicolenus
90	5	62.5	230	8	Q94RG5	Q94rg5	heterodontu
91	5	62.5	230	8	Q9G6R0	Q9g6r0	diplophos t
92	5	62.5	230	8	Q94TB6	Q94tb6	neoscopelus
93	5	62.5	230	8	Q9B9V2	Q9b9v2	aulopus jap
94	5	62.5	230	8	Q94SA0	Q94sa0	elassoma ev
95	5	62.5	230	8	Q9G6T4	Q9g6t4	sardinops m
96	5	62.5	230	8	Q94TG6	Q94tg6	ijimaia dof
97	5	62.5	230	8	Q95LI2	Q95li2	oncorhynchu
98	5	62.5	230	8	Q94TF3	Q94tf3	chlorophtha
99	5	62.5	230	8	Q94YS1	Q94ys1	engraulis j
100	5	62.5	230	8	Q94S74	Q94s74	stephanolep
101	5	62.5	230	8	Q94SX1	Q94sx1	exocoetus v
102	5	62.5	230	8	Q9G6P7	Q9g6p7	polymixia j
103	5	62.5	230	8	Q94T64	Q94t64	trachipteru
104	5	62.5	230	8	Q94SQ6	Q94sq6	hoplostethu
105	5	62.5	230	8	Q94YP2	Q94yp2	pantodon bu
106	5	62.5	230	8	Q94SL7	Q94sl7	zeus faber
107	5	62.5	230	8	Q94T51	Q94t51	zu cristatu
108	5	62.5	230	8	Q9B606	Q9b606	plecoglossu
109	5	62.5	230	8	Q9G6S0	Q9g6s0	coregonus l
110	5	62.5	230	8	Q8HMOV2	Q8hmv2	gymnothorax
111	5	62.5	230	8	Q8HML8	Q8hml8	hiodon alos
112	5	62.5	230	8	Q8HMK5	Q8hmk5	aphredoderu
113	5	62.5	230	8	Q8HMH9	Q8hmh9	bassozetus
114	5	62.5	230	8	Q8HMF3	Q8hmf3	cataetys ru

115	5	62.5	230	8	Q8HME0	Q8hme0	diplacantho
116	5	62.5	230	8	Q8HMB4	Q8hmb4	melanonus z
117	5	62.5	230	8	Q8HM63	Q8hm63	lophius ame
118	5	62.5	230	8	Q8HM50	Q8hm50	chaunax abe
119	5	62.5	230	8	Q8HM37	Q8hm37	chaunax tos
120	5	62.5	230	8	Q8HM24	Q8hm24	caulophryne
121	5	62.5	230	8	Q8HM11	Q8hml1	melanocetus
122	5	62.5	230	8	Q8HLZ8	Q8hlz8	melanotaeni
123	5	62.5	230	8	Q8HLY5	Q8hly5	hypoatherin
124	5	62.5	230	8	Q8HLX2	Q8hlx2	oryzias lat
125	5	62.5	230	8	Q8HLU7	Q8hlu7	cetostoma r
126	5	62.5	230	8	Q8HLT4	Q8hlt4	eutaeniopho
127	5	62.5	230	8	Q8HLS1	Q8hls1	anoplogaste
128	5	62.5	230	8	Q8HLN2	Q8hln2	anomalops k
129	5	62.5	230	8	Q8HLL9	Q8hll9	monocentris
130	5	62.5	230	8	Q8HLK6	Q8hlk6	beryx decad
131	5	62.5	230	8	Q8HLJ3	Q8hlj3	ostichthys
132	5	62.5	230	8	Q8HLI0	Q8hli0	sargocentro
133	5	62.5	230	8	Q8HLF4	Q8hlf4	zenion japo
134	5	62.5	230	8	Q8HLE1	Q8hle1	allocyttus
135	5	62.5	230	8	Q8HLC8	Q8hlc8	neocyttus r
136	5	62.5	230	8	Q8HLA2	Q8hla2	indostomus
137	5	62.5	230	8	Q8HL64	Q8hl64	satyrichthy
138	5	62.5	230	8	Q8HKZ9	Q8hkhz9	emmelichthy
139	5	62.5	230	8	Q8HKY6	Q8hky6	pteroaesio
140	5	62.5	230	8	Q8HKW0	Q8hkw0	enedrias cr
141	5	62.5	230	8	Q8HKT4	Q8hkt4	salarias fa
142	5	62.5	230	8	Q8HKS1	Q8hks1	arcos sp. k
143	5	62.5	230	8	Q8HKP5	Q8hkp5	rhyacichthy
144	5	62.5	230	8	Q8HKN2	Q8hkn2	eleotris ac
145	5	62.5	230	8	Q8HKL9	Q8hkl9	sufflamen f
146	5	62.5	230	8	Q8HCW2	Q8hwc2	fugu rubrip
147	5	62.5	230	8	Q85UE8	Q85ue8	euthynnus a
148	5	62.5	230	8	Q85IP2	Q85ip2	cyprinus ca
149	5	62.5	230	8	Q85IP1	Q85ip1	cyprinus ca
150	5	62.5	230	8	Q85IP0	Q85ip0	cyprinus ca
151	5	62.5	230	8	Q85E83	Q85e83	sarcocheili
152	5	62.5	230	8	Q85E32	Q85e32	phenacogram
153	5	62.5	230	8	Q85E20	Q85e20	chalceus ma
154	5	62.5	230	8	Q85E07	Q85e07	eigenmannia
155	5	62.5	230	8	Q85D95	Q85d95	alepocephal
156	5	62.5	230	8	Q85D82	Q85d82	bathylagus
157	5	62.5	230	8	Q85D43	Q85d43	galaxias ma
158	5	62.5	230	8	Q85D30	Q85d30	glossanodon
159	5	62.5	230	8	Q85D17	Q85d17	nansenia ar
160	5	62.5	230	8	Q85D04	Q85d04	platytrocte
161	5	62.5	230	8	Q85CZ1	Q85cz1	retropinna
162	5	62.5	230	8	Q85CX8	Q85cx8	salangichth
163	5	62.5	230	8	Q85CW5	Q85cw5	opisthoproc
164	5	62.5	230	8	Q85BZ2	Q85bz2	cyprinus ca
165	5	62.5	230	8	Q7YFF0	Q7yff0	thunnus thy
166	5	62.5	230	8	Q7YDB0	Q7ydb0	thunnus thy
167	5	62.5	230	8	Q7YC39	Q7yc39	etheostoma
168	5	62.5	230	10	Q8LCV1	Q8lcv1	arabidopsis
169	5	62.5	231	8	Q85MC4	Q85mc4	monoblephar
170	5	62.5	232	8	Q8HN46	Q8hn46	brugia mala
171	5	62.5	232	10	Q9ZQH0	Q9zqh0	arabidopsis

172	5	62.5	234	8	Q94XJ4	Q94xj4 neoceratodu
173	5	62.5	234	10	Q9FJZ8	Q9fjz8 arabidopsis
174	5	62.5	243	5	O17308	O17308 tribolium c
175	5	62.5	246	5	Q9VL11	Q9vl11 drosophila
176	5	62.5	246	5	Q8T9L2	Q8t9l2 drosophila
177	5	62.5	247	11	Q60965	Q60965 mus musculu
178	5	62.5	247	11	Q8C2Q0	Q8c2q0 mus musculu
179	5	62.5	255	5	Q8T9V7	Q8t9v7 aedes aegyp
180	5	62.5	262	10	O24503	O24503 muhlenbergi
181	5	62.5	279	2	Q9AET1	Q9aet1 aeromonas h
182	5	62.5	284	16	Q8G264	Q8g264 brucella su
183	5	62.5	288	10	Q9LZ55	Q9lzf55 arabidopsis
184	5	62.5	292	10	Q9FNY3	Q9fny3 arabidopsis
185	5	62.5	301	5	Q8MRL9	Q8mrl9 drosophila
186	5	62.5	309	10	Q7XP75	Q7xp75 oryza sativ
187	5	62.5	313	10	Q93WT3	Q93wt3 sorghum bic
188	5	62.5	316	16	Q8FSV0	Q8fsv0 corynebacte
189	5	62.5	317	10	Q8VXN6	Q8vxn6 coleochaete
190	5	62.5	317	16	Q8NL52	Q8nl52 corynebacte
191	5	62.5	318	10	Q84K50	Q84k50 arabidopsis
192	5	62.5	319	16	Q8F1C0	Q8f1c0 leptospira
193	5	62.5	320	16	Q8YFQ4	Q8yfq4 brucella me
194	5	62.5	320	17	Q8TS69	Q8ts69 methanosarc
195	5	62.5	320	17	Q8PVB7	Q8pvb7 methanosarc
196	5	62.5	323	5	Q9VL80	Q9vl80 drosophila
197	5	62.5	333	16	Q81RT8	Q81rt8 bacillus an
198	5	62.5	334	16	Q82L34	Q82l34 streptomyce
199	5	62.5	338	5	Q9VPU4	Q9vpu4 drosophila
200	5	62.5	362	16	Q89ZF7	Q89zf7 bacteroides
201	5	62.5	363	10	Q43032	Q43032 petroselinu
202	5	62.5	364	5	Q95T75	Q95t75 drosophila
203	5	62.5	366	16	Q9K1U7	Q9klu7 chlamydia p
204	5	62.5	369	16	Q9Z839	Q9z839 chlamydia p
205	5	62.5	370	10	Q9LYK0	Q9lyk0 arabidopsis
206	5	62.5	371	16	Q9RRJ3	Q9rrj3 deinococcus
207	5	62.5	373	2	Q9F2H7	Q9f2h7 staphylococ
208	5	62.5	375	16	Q9Z6X8	Q9z6x8 chlamydia p
209	5	62.5	381	16	Q88W94	Q88w94 lactobacill
210	5	62.5	384	16	Q7VPZ4	Q7vpz4 chlamydia p
211	5	62.5	384	16	Q7VEH7	Q7veh7 prochloroco
212	5	62.5	395	5	Q9VEK3	Q9vek3 drosophila
213	5	62.5	396	16	Q8Y3L8	Q8y3l8 listeria mo
214	5	62.5	399	11	Q8BZF1	Q8bzf1 mus musculu
215	5	62.5	400	16	Q7US24	Q7us24 rhodopirell
216	5	62.5	401	9	Q7Y4B3	Q7y4b3 bacterioph
217	5	62.5	404	16	Q9CML0	Q9cml0 pasteurella
218	5	62.5	408	16	O66985	O66985 aquifex aeo
219	5	62.5	408	16	Q8K5E6	Q8k5e6 chlorobium
220	5	62.5	419	10	Q8LMI1	Q8lmi1 oryza sativ
221	5	62.5	427	10	O23188	O23188 arabidopsis
222	5	62.5	427	10	Q94AQ0	Q94aq0 arabidopsis
223	5	62.5	430	3	O13699	O13699 schizosacch
224	5	62.5	431	12	Q9Q8P7	Q9q8p7 myxoma viru
225	5	62.5	432	12	Q9Q922	Q9q922 shope fibro
226	5	62.5	432	16	Q8ENB7	Q8enb7 oceanobacil
227	5	62.5	443	2	Q842C0	Q842c0 escherichia
228	5	62.5	450	5	Q8I2P5	Q8i2p5 plasmodium

229	5	62.5	453	16	O66852	O66852 aquifex aeo
230	5	62.5	454	5	Q961R4	Q961r4 drosophila
231	5	62.5	461	4	Q7Z4J7	Q7z4j7 homo sapien
232	5	62.5	461	10	Q84M71	Q84m71 oryza sativ
233	5	62.5	462	10	Q8H2D1	Q8h2d1 arabidopsis
234	5	62.5	463	3	Q8WZN5	Q8wzn5 pleurotus o
235	5	62.5	468	16	Q8RDQ8	Q8rdq8 fusobacteri
236	5	62.5	469	5	Q8IQW6	Q8iqw6 drosophila
237	5	62.5	470	16	Q7U238	Q7u238 mycobacteri
238	5	62.5	472	16	Q89Z59	Q89z59 bacteroides
239	5	62.5	477	16	Q8RCS3	Q8rcs3 thermoanaer
240	5	62.5	478	10	O81779	O81779 arabidopsis
241	5	62.5	478	16	Q88FB1	Q88fb1 pseudomonas
242	5	62.5	484	10	Q7XWI6	Q7xwi6 oryza sativ
243	5	62.5	485	5	Q9NA31	Q9na31 caenorhabdi
244	5	62.5	487	5	Q8T368	Q8t368 ostertagia
245	5	62.5	488	5	Q9V630	Q9v630 drosophila
246	5	62.5	489	5	Q9TWZ1	Q9twz1 drosophila
247	5	62.5	492	5	Q8T093	Q8t093 drosophila
248	5	62.5	494	5	Q9XZW0	Q9xzw0 heliothis v
249	5	62.5	494	16	Q8YJQ7	Q8yjq7 brucella me
250	5	62.5	494	16	Q8FY45	Q8fy45 brucella su
251	5	62.5	496	5	O18468	O18468 heliothis v
252	5	62.5	502	16	Q92L01	Q92l01 rhizobium m
253	5	62.5	508	5	Q95Y52	Q95y52 caenorhabdi
254	5	62.5	509	16	Q8XVG1	Q8xvg1 ralstonia s
255	5	62.5	519	13	Q9PTY6	Q9pty6 anguilla ja
256	5	62.5	519	13	Q9PTY7	Q9pty7 anguilla ja
257	5	62.5	521	13	Q8QGI8	Q8qgi8 anguilla an
258	5	62.5	541	5	Q9U9B8	Q9u9b8 ceratitidis c
259	5	62.5	550	5	O17145	O17145 lucilia cup
260	5	62.5	572	5	Q8MRU3	Q8mru3 drosophila
261	5	62.5	572	5	Q9VYL1	Q9vyl1 drosophila
262	5	62.5	582	3	Q96UP6	Q96up6 emericella
263	5	62.5	585	5	Q8IQB5	Q8iqb5 drosophila
264	5	62.5	606	5	Q9BLY8	Q9bly8 drosophila
265	5	62.5	615	5	P91573	P91573 caenorhabdi
266	5	62.5	633	16	Q9I408	Q9i408 pseudomonas
267	5	62.5	640	11	Q8BTV5	Q8btv5 mus musculu
268	5	62.5	651	5	Q9VFA9	Q9vfa9 drosophila
269	5	62.5	655	4	Q8IZ32	Q8iz32 homo sapien
270	5	62.5	655	4	Q7Z6J4	Q7z6j4 homo sapien
271	5	62.5	655	16	Q81DA4	Q81da4 bacillus ce
272	5	62.5	658	5	O97472	O97472 caenorhabdi
273	5	62.5	693	13	Q98SG0	Q98sg0 xenopus lae
274	5	62.5	695	13	Q98SF9	Q98sf9 xenopus lae
275	5	62.5	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
276	5	62.5	703	16	Q81JV4	Q81jv4 bacillus an
277	5	62.5	703	16	Q814S5	Q814s5 bacillus ce
278	5	62.5	715	16	Q8YS58	Q8ys58 anabaena sp
279	5	62.5	725	10	Q7XF80	Q7xf80 oryza sativ
280	5	62.5	743	10	Q9SLB2	Q9slb2 arabidopsis
281	5	62.5	747	13	Q91963	Q91963 xenopus. ap
282	5	62.5	853	11	Q8CB40	Q8cb40 mus musculu
283	5	62.5	855	16	P73546	P73546 synechocyst
284	5	62.5	859	3	Q9HFI9	Q9hfi9 neurospora
285	5	62.5	930	5	Q8SWW0	Q8sww0 drosophila

286	5	62.5	938	10	O04660	O04660 arabidopsis
287	5	62.5	944	16	Q8PGQ7	Q8pgq7 xanthomonas
288	5	62.5	944	16	Q8PCR7	Q8pcr7 xanthomonas
289	5	62.5	947	10	O04494	O04494 arabidopsis
290	5	62.5	963	5	Q9GPM9	Q9gpm9 caenorhabdi
291	5	62.5	996	5	Q27461	Q27461 caenorhabdi
292	5	62.5	996	5	P90735	P90735 caenorhabdi
293	5	62.5	1007	17	Q9YF24	Q9yf24 aeropyrum p
294	5	62.5	1039	5	Q9VWG8	Q9vwg8 drosophila
295	5	62.5	1049	11	Q80TY4	Q80ty4 mus musculu
296	5	62.5	1061	17	Q8TM82	Q8tm82 methanosarc
297	5	62.5	1069	11	O54963	O54963 rattus norv
298	5	62.5	1075	10	Q9LNP5	Q9lnp5 arabidopsis
299	5	62.5	1092	16	Q8ZN12	Q8zn12 salmonella
300	5	62.5	1160	16	Q8XT75	Q8xt75 ralstonia s
301	5	62.5	1180	17	Q8TI57	Q8ti57 methanosarc
302	5	62.5	1209	10	Q94FG7	Q94fg7 chlamydomon
303	5	62.5	1241	5	Q9V505	Q9v505 drosophila
304	5	62.5	1247	5	Q8SRK6	Q8srk6 encephalito
305	5	62.5	1247	10	Q8H7X8	Q8h7x8 oryza sativ
306	5	62.5	1270	5	Q9GPN0	Q9gpn0 caenorhabdi
307	5	62.5	1290	2	Q48756	Q48756 leuconostoc
308	5	62.5	1313	4	Q9HCK6	Q9hck6 homo sapien
309	5	62.5	1334	5	Q9XTS7	Q9xts7 caenorhabdi
310	5	62.5	1386	17	Q8TI72	Q8ti72 methanosarc
311	5	62.5	1412	13	Q8UW84	Q8uw84 paralichthy
312	5	62.5	1418	13	O93457	O93457 scophthalmu
313	5	62.5	1418	13	Q8UW83	Q8uw83 paralichthy
314	5	62.5	1449	10	Q94DD5	Q94dd5 oryza sativ
315	5	62.5	1496	5	Q9NFV5	Q9nfv5 drosophila
316	5	62.5	1496	5	Q9VIT9	Q9vit9 drosophila
317	5	62.5	1564	5	Q9XW49	Q9xw49 caenorhabdi
318	5	62.5	1630	10	Q8H3L8	Q8h3l8 oryza sativ
319	5	62.5	1640	12	Q80J95	Q80j95 murine noro
320	5	62.5	1743	4	Q9BYP7	Q9byp7 homo sapien
321	5	62.5	1800	4	Q8TCX6	Q8tcx6 homo sapien
322	5	62.5	1816	5	Q8IJL6	Q8ijl6 plasmodium
323	5	62.5	1876	2	Q9R686	Q9r686 bacillus su
324	5	62.5	2245	5	Q86A36	Q86a36 dictyosteli
325	5	62.5	2262	5	Q9V4P4	Q9v4p4 drosophila
326	5	62.5	2480	5	Q86MR6	Q86mr6 plasmodium
327	5	62.5	3103	5	Q9GV77	Q9gv77 lytechinus
328	5	62.5	3190	2	Q93NW7	Q93nw7 streptomyce
329	5	62.5	3192	2	Q9L4W4	Q9l4w4 streptomyce
330	5	62.5	3351	5	Q9V496	Q9v496 drosophila
331	5	62.5	3351	5	Q94907	Q94907 drosophila
332	5	62.5	4450	2	Q44928	Q44928 bacillus br
333	5	62.5	6048	2	Q93H87	Q93h87 streptomyce
334	5	62.5	7746	16	Q82QT4	Q82qt4 streptomyce
335	4	50.0	19	4	Q9UCC8	Q9ucc8 homo sapien
336	4	50.0	21	4	Q9UCC3	Q9ucc3 homo sapien
337	4	50.0	24	5	Q9U9B7	Q9u9b7 ceratitidis c
338	4	50.0	28	4	Q9UCD1	Q9ucd1 homo sapien
339	4	50.0	30	4	Q9UCA9	Q9uca9 homo sapien
340	4	50.0	30	11	Q9QV42	Q9qv42 rattus sp.
341	4	50.0	33	4	Q9UC33	Q9uc33 homo sapien
342	4	50.0	34	17	Q9HMS8	Q9hms8 halobacteri



343	4	50.0	36	16	Q8EIW6	Q8eiw6 shewanella
344	4	50.0	38	4	Q9NRW8	Q9nrw8 homo sapien
345	4	50.0	41	2	O31327	O31327 bacillus br
346	4	50.0	43	16	Q88YU4	Q88yu4 lactobacill
347	4	50.0	44	2	Q47324	Q47324 escherichia
348	4	50.0	44	16	Q8E9C1	Q8e9c1 shewanella
349	4	50.0	46	13	Q98UE4	Q98ue4 xenopus lae
350	4	50.0	46	16	Q88UM4	Q88um4 lactobacill
351	4	50.0	46	16	Q7VNN1	Q7vnn1 haemophilus
352	4	50.0	47	10	Q7XS03	Q7xs03 oryza sativ
353	4	50.0	47	16	Q8E9U6	Q8e9u6 shewanella
354	4	50.0	50	16	Q7UKK2	Q7ukk2 rhodopirell
355	4	50.0	51	16	Q8G1Q7	Q8glq7 brucella su
356	4	50.0	52	7	Q9XR67	Q9xr67 oncorhynch
357	4	50.0	52	7	Q9XR64	Q9xr64 oncorhynch
358	4	50.0	52	7	Q9XR66	Q9xr66 oncorhynch
359	4	50.0	52	7	Q9XR65	Q9xr65 oncorhynch
360	4	50.0	53	12	Q8V3J3	Q8v3j3 swinepox vi
361	4	50.0	53	16	Q81TE4	Q81te4 bacillus an
362	4	50.0	53	16	Q81G86	Q81g86 bacillus ce
363	4	50.0	53	16	Q7UMV1	Q7umv1 rhodopirell
364	4	50.0	54	10	Q8GWS1	Q8gws1 arabidopsis
365	4	50.0	58	4	Q8WYD6	Q8wyd6 homo sapien
366	4	50.0	59	5	Q8ISA4	Q8isa4 plasmodium
367	4	50.0	60	5	Q9BMS3	Q9bms3 plasmodium
368	4	50.0	60	16	Q7VDW8	Q7vdw8 prochloroco
369	4	50.0	61	16	Q9KPP8	Q9kpp8 vibrio chol
370	4	50.0	62	5	Q9BJJ6	Q9bjj6 plasmodium
371	4	50.0	62	5	Q9BJJ4	Q9bjj4 plasmodium
372	4	50.0	62	10	Q9XF78	Q9xf78 oryza sativ
373	4	50.0	63	17	Q8ZY13	Q8zy13 pyrobaculum
374	4	50.0	64	13	Q8AXL3	Q8axl3 micropterus
375	4	50.0	65	5	Q8IH85	Q8ih85 drosophila
376	4	50.0	65	11	O54696	O54696 mus musculu
377	4	50.0	66	12	Q8QIA7	Q8qia7 hepatitis c
378	4	50.0	67	9	Q7Y3X4	Q7y3x4 bacterioph
379	4	50.0	68	2	Q9AFY2	Q9afy2 shigella fl
380	4	50.0	68	5	Q9BL96	Q9bl96 caenorhabdi
381	4	50.0	69	8	Q36132	Q36132 tuberaphis
382	4	50.0	69	16	Q9WY53	Q9wy53 thermotoga
383	4	50.0	71	2	Q9AE14	Q9ael4 acetobacter
384	4	50.0	71	6	Q29305	Q29305 sus scrofa
385	4	50.0	71	16	Q9JQW9	Q9jqw9 neisseria m
386	4	50.0	71	16	Q8FLH2	Q8flh2 corynebacte
387	4	50.0	72	2	Q44953	Q44953 bacillus br
388	4	50.0	72	9	Q855R4	Q855r4 mycobacteri
389	4	50.0	72	9	Q855G5	Q855g5 mycobacteri
390	4	50.0	72	16	Q8PGL2	Q8pgl2 xanthomonas
391	4	50.0	72	16	Q8CVC8	Q8cvc8 streptococc
392	4	50.0	73	16	Q9PFQ5	Q9pfq5 xylella fas
393	4	50.0	73	16	Q87BA9	Q87ba9 xylella fas
394	4	50.0	74	10	Q9XIR8	Q9xir8 arabidopsis
395	4	50.0	74	16	Q92A64	Q92a64 listeria in
396	4	50.0	74	16	Q8Y5W1	Q8y5w1 listeria mo
397	4	50.0	74	16	Q7UQ30	Q7uq30 rhodopirell
398	4	50.0	74	17	Q9HQU2	Q9hqu2 halobacteri
399	4	50.0	75	9	Q38636	Q38636 bacterioph



400	4	50.0	75	9	Q38648	Q38648 bacterioph
401	4	50.0	75	16	Q9PDG5	Q9pdg5 xylella fas
402	4	50.0	75	16	Q97LV7	Q97lv7 clostridium
403	4	50.0	75	16	Q92HH8	Q92hh8 rickettsia
404	4	50.0	75	16	Q8PID2	Q8pid2 xanthomonas
405	4	50.0	75	16	Q8P718	Q8p718 xanthomonas
406	4	50.0	75	16	Q87UE9	Q87ue9 pseudomonas
407	4	50.0	75	16	Q87UB3	Q87ub3 pseudomonas
408	4	50.0	75	16	Q87DN9	Q87dn9 xylella fas
409	4	50.0	75	16	Q7VCN1	Q7vcn1 prochloroco
410	4	50.0	76	9	Q38628	Q38628 bacterioph
411	4	50.0	76	9	Q38626	Q38626 bacterioph
412	4	50.0	76	15	Q991R9	Q991r9 human immun
413	4	50.0	76	15	Q991R8	Q991r8 human immun
414	4	50.0	77	17	O26981	O26981 methanobact
415	4	50.0	78	5	Q9NFF6	Q9nff6 plasmodium
416	4	50.0	78	16	Q81E52	Q81e52 bacillus ce
417	4	50.0	78	17	Q9HNM4	Q9hnm4 halobacteri
418	4	50.0	79	2	Q8KIY2	Q8kiy2 lactococcus
419	4	50.0	81	9	Q8HAI0	Q8hai0 salmonella
420	4	50.0	81	11	Q9D2G3	Q9d2g3 mus musculu
421	4	50.0	81	13	Q98TN9	Q98tn9 platichthys
422	4	50.0	81	16	Q8ESV9	Q8esv9 oceanobacil
423	4	50.0	82	4	Q9UI77	Q9ui77 homo sapien
424	4	50.0	82	11	Q8VI12	Q8vil2 mus musculu
425	4	50.0	82	16	Q8ZEE2	Q8zee2 yersinia pe
426	4	50.0	84	2	Q9RN90	Q9rn90 salmonella
427	4	50.0	84	5	Q9VS22	Q9vs22 drosophila
428	4	50.0	84	9	Q38141	Q38141 bacterioph
429	4	50.0	84	16	Q81R87	Q81r87 bacillus an
430	4	50.0	85	5	Q86CT3	Q86ct3 branchiosto
431	4	50.0	85	10	Q9LF86	Q9lf86 arabidopsis
432	4	50.0	85	12	Q8VB15	Q8vb15 white spot
433	4	50.0	85	16	Q7VHS8	Q7vhs8 helicobacte
434	4	50.0	86	1	Q9C4V4	Q9c4v4 sulfolobus
435	4	50.0	87	2	Q9RBR8	Q9rbr8 pseudomonas
436	4	50.0	87	5	Q9GS26	Q9gs26 ancylostoma
437	4	50.0	87	5	Q21171	Q21171 caenorhabdi
438	4	50.0	88	12	Q9IF56	Q9if56 human enter
439	4	50.0	88	16	Q7VAW2	Q7vaw2 prochloroco
440	4	50.0	89	6	Q9TS76	Q9ts76 bos taurus
441	4	50.0	89	7	O62863	O62863 gallus gall
442	4	50.0	89	7	O19500	O19500 gallus gall
443	4	50.0	89	7	O19492	O19492 gallus gall
444	4	50.0	89	12	Q9IF57	Q9if57 human enter
445	4	50.0	89	12	Q80H65	Q80h65 human coxs
446	4	50.0	90	5	Q8WST0	Q8wst0 ciona intes
447	4	50.0	90	5	Q9W5F9	Q9w5f9 drosophila
448	4	50.0	90	9	Q853U5	Q853u5 mycobacteri
449	4	50.0	90	11	P70443	P70443 mus musculu
450	4	50.0	90	16	Q9K0N3	Q9k0n3 neisseria m
451	4	50.0	90	16	Q9JVQ8	Q9jvq8 neisseria m
452	4	50.0	90	16	Q8YBH5	Q8ybh5 brucella me
453	4	50.0	90	16	Q8FWX0	Q8fwx0 brucella su
454	4	50.0	90	16	Q7UTU7	Q7utu7 rhodopirell
455	4	50.0	91	7	Q7YP43	Q7yp43 cervus nipp
456	4	50.0	91	7	Q7YP42	Q7yp42 cervus nipp

457	4	50.0	91	12	Q9IF55	Q9if55 human enter
458	4	50.0	91	16	Q8F784	Q8f784 leptospira
459	4	50.0	91	16	Q89LY8	Q89ly8 bradyrhizob
460	4	50.0	92	2	Q9KJF5	Q9kjf5 thauera aro
461	4	50.0	92	5	Q8IS88	Q8is88 trypanosoma
462	4	50.0	92	5	Q7YZC6	Q7yzc6 trypanosoma
463	4	50.0	92	5	Q7YZC5	Q7yzc5 trypanosoma
464	4	50.0	92	9	O64108	O64108 bacterioph
465	4	50.0	92	16	O34730	O34730 bacillus su
466	4	50.0	92	16	Q7WKG7	Q7wkg7 bordetella
467	4	50.0	92	16	Q7W922	Q7w922 bordetella
468	4	50.0	92	17	O30237	O30237 archaeoglob
469	4	50.0	93	5	Q21047	Q21047 caenorhabdi
470	4	50.0	94	2	Q8VRZ7	Q8vrz7 shigella fl
471	4	50.0	94	5	P81260	P81260 plasmodium
472	4	50.0	94	10	Q84PF2	Q84pf2 gossypium h
473	4	50.0	94	10	Q84PF1	Q84pf1 gossypium r
474	4	50.0	94	10	Q84PF0	Q84pf0 gossypium b
475	4	50.0	94	10	Q84PE9	Q84pe9 gossypium b
476	4	50.0	94	10	Q84PE8	Q84pe8 gossypioide
477	4	50.0	94	16	Q88YV3	Q88yv3 lactobacill
478	4	50.0	94	16	Q87MS7	Q87ms7 vibrio para
479	4	50.0	95	5	Q94751	Q94751 schistosoma
480	4	50.0	95	9	Q858U1	Q858u1 bacterioph
481	4	50.0	95	15	P90439	P90439 human immun
482	4	50.0	95	15	P90440	P90440 human immun
483	4	50.0	95	15	P89570	P89570 human immun
484	4	50.0	95	15	P89571	P89571 human immun
485	4	50.0	95	15	P89582	P89582 human immun
486	4	50.0	95	15	Q7ZRM5	Q7zrm5 chimpanzee
487	4	50.0	95	15	Q7ZRM4	Q7zrm4 chimpanzee
488	4	50.0	95	15	Q7ZRM3	Q7zrm3 chimpanzee
489	4	50.0	95	15	Q7ZRM2	Q7zrm2 chimpanzee
490	4	50.0	95	15	Q7ZRM1	Q7zrm1 chimpanzee
491	4	50.0	95	15	Q7ZRM0	Q7zrm0 chimpanzee
492	4	50.0	95	15	Q7ZRL9	Q7zrl9 chimpanzee
493	4	50.0	95	15	Q7ZRL8	Q7zrl8 chimpanzee
494	4	50.0	95	15	Q7ZRL7	Q7zrl7 chimpanzee
495	4	50.0	95	15	Q7ZRL6	Q7zrl6 chimpanzee
496	4	50.0	95	16	Q8EVE5	Q8eve5 mycoplasma
497	4	50.0	96	2	Q8VSK4	Q8vsk4 shigella fl
498	4	50.0	96	2	Q9AFU9	Q9afu9 shigella fl
499	4	50.0	96	10	Q8GSC3	Q8gsc3 oryza sativ
500	4	50.0	96	16	Q89U21	Q89u21 bradyrhizob
501	4	50.0	96	17	Q8TI75	Q8ti75 methanosarc
502	4	50.0	97	5	O02114	O02114 caenorhabdi
503	4	50.0	97	16	Q8ECY5	Q8ecy5 shewanella
504	4	50.0	97	16	Q8A4Z9	Q8a4z9 bacteroides
505	4	50.0	98	5	Q9GP45	Q9gp45 drosophila
506	4	50.0	98	16	Q8PCV6	Q8pcv6 xanthomonas
507	4	50.0	99	13	Q9PSS3	Q9pss3 gallus gall
508	4	50.0	99	16	Q7UMF6	Q7umf6 rhodopirell
509	4	50.0	99	17	Q8ZTT7	Q8ztt7 pyrobaculum
510	4	50.0	100	5	Q9U2F4	Q9u2f4 caenorhabdi
511	4	50.0	100	11	Q8C8T4	Q8c8t4 mus musculu
512	4	50.0	100	12	Q91LA4	Q91la4 white spot
513	4	50.0	101	3	Q96U65	Q96u65 neurospora

514	4	50.0	101	12	Q9IZR8	Q9izr8 tick-borne
515	4	50.0	101	12	Q80PA8	Q80pa8 spodoptera
516	4	50.0	103	10	Q7XU26	Q7xu26 oryza sativ
517	4	50.0	103	16	Q8FH22	Q8fh22 escherichia
518	4	50.0	103	16	O84895	O84895 salmonella
519	4	50.0	104	5	Q9GP72	Q9gp72 drosophila
520	4	50.0	104	5	Q9GP75	Q9gp75 drosophila
521	4	50.0	104	5	Q9GN84	Q9gn84 drosophila
522	4	50.0	104	5	Q9GN82	Q9gn82 drosophila
523	4	50.0	104	5	Q9GN83	Q9gn83 drosophila
524	4	50.0	104	8	Q8SLI8	Q8sli8 dunaliella
525	4	50.0	104	10	Q84XQ7	Q84xq7 brassica ra
526	4	50.0	104	12	Q80GB9	Q80gb9 human coxs
527	4	50.0	104	16	Q97P68	Q97p68 streptococc
528	4	50.0	104	16	Q8DNP9	Q8dnp9 streptococc
529	4	50.0	104	16	Q835H2	Q835h2 enterococcu
530	4	50.0	105	3	O13706	O13706 schizosacch
531	4	50.0	105	5	Q9GP79	Q9gp79 drosophila
532	4	50.0	105	5	Q9GP78	Q9gp78 drosophila
533	4	50.0	105	5	Q9GNH2	Q9gnh2 drosophila
534	4	50.0	105	12	Q7T5F7	Q7t5f7 antheraea p
535	4	50.0	105	16	Q8YQ72	Q8yq72 anabaena sp
536	4	50.0	105	16	Q8ZQG4	Q8zqg4 salmonella
537	4	50.0	105	16	Q88G02	Q88g02 pseudomonas
538	4	50.0	106	5	Q9GP80	Q9gp80 drosophila
539	4	50.0	106	16	Q8XSX7	Q8xsx7 ralstonia s
540	4	50.0	106	16	Q8E803	Q8e803 shewanella
541	4	50.0	107	12	Q80GJ3	Q80gj3 human enter
542	4	50.0	107	12	Q80GH8	Q80gh8 human coxs
543	4	50.0	107	12	Q80GC2	Q80gc2 human coxs
544	4	50.0	107	16	Q8G636	Q8g636 bifidobacte
545	4	50.0	108	12	Q80GC0	Q80gc0 human coxs
546	4	50.0	108	16	Q8PM18	Q8pml8 xanthomonas
547	4	50.0	109	10	Q8W4S0	Q8w4s0 arabidopsis
548	4	50.0	109	11	Q61064	Q61064 mus musculu
549	4	50.0	109	16	Q8ZQ87	Q8zq87 salmonella
550	4	50.0	110	9	Q9ZWZ9	Q9zww9 mycobacteri
551	4	50.0	110	10	Q93XD0	Q93xd0 ze mays (m
552	4	50.0	110	10	Q8H429	Q8h429 oryza sativ
553	4	50.0	111	2	Q8KJB4	Q8kjb4 rhizobium l
554	4	50.0	111	2	Q9RIH2	Q9rih2 xenorhabdus
555	4	50.0	111	2	Q9F8D1	Q9f8d1 rhizobium e
556	4	50.0	111	12	Q8VA98	Q8va98 white spot
557	4	50.0	111	12	Q80GH9	Q80gh9 human coxs
558	4	50.0	111	12	Q80GC1	Q80gc1 human coxs
559	4	50.0	111	16	Q8PAC7	Q8pac7 xanthomonas
560	4	50.0	111	16	Q7VKT5	Q7vkt5 haemophilus
561	4	50.0	111	16	Q7V725	Q7v725 prochloroco
562	4	50.0	112	12	Q80GJ1	Q80gj1 human enter
563	4	50.0	112	12	Q80GB8	Q80gb8 human coxs
564	4	50.0	112	12	Q80GB6	Q80gb6 human coxs
565	4	50.0	112	16	Q98IK9	Q98ik9 rhizobium l
566	4	50.0	112	16	Q8ZN06	Q8zn06 salmonella
567	4	50.0	112	16	Q87LW5	Q87lw5 vibrio para
568	4	50.0	112	16	Q82E60	Q82e60 streptomyce
569	4	50.0	113	10	Q9M3N2	Q9m3n2 vicia faba
570	4	50.0	113	12	Q9IX40	Q9ix40 human enter

571	4	50.0	113	12	Q9IX31	Q9ix31 human enter
572	4	50.0	113	12	Q9IX34	Q9ix34 human enter
573	4	50.0	113	12	Q9IX45	Q9ix45 human enter
574	4	50.0	113	12	Q9IX46	Q9ix46 human enter
575	4	50.0	113	12	Q9IX44	Q9ix44 human enter
576	4	50.0	113	12	Q9IX47	Q9ix47 human enter
577	4	50.0	113	12	Q9IX52	Q9ix52 human enter
578	4	50.0	113	12	Q9IX33	Q9ix33 human enter
579	4	50.0	113	12	Q9IX50	Q9ix50 human enter
580	4	50.0	113	12	Q9IX42	Q9ix42 human enter
581	4	50.0	113	12	Q9IX39	Q9ix39 human enter
582	4	50.0	113	12	Q9IX43	Q9ix43 human enter
583	4	50.0	113	12	Q9IX49	Q9ix49 human enter
584	4	50.0	113	12	Q9IX48	Q9ix48 human enter
585	4	50.0	113	12	Q9IX41	Q9ix41 human enter
586	4	50.0	113	12	Q9IX32	Q9ix32 human enter
587	4	50.0	113	12	Q9IX51	Q9ix51 human enter
588	4	50.0	113	12	Q80GJ2	Q80gj2 human enter
589	4	50.0	113	16	Q89W55	Q89w55 bradyrhizob
590	4	50.0	114	10	Q9FKC5	Q9fkc5 arabidopsis
591	4	50.0	115	2	Q8VMD4	Q8vmd4 pseudanabae
592	4	50.0	115	15	Q74763	Q74763 human immun
593	4	50.0	115	15	O90619	O90619 human immun
594	4	50.0	115	16	Q8U5F4	Q8u5f4 agrobacteri
595	4	50.0	115	17	Q9HNY1	Q9hny1 halobacteri
596	4	50.0	116	2	Q9FA31	Q9fa31 salmonella
597	4	50.0	116	10	Q9AT59	Q9at59 lolium pere
598	4	50.0	117	4	Q7Z6X4	Q7z6x4 homo sapien
599	4	50.0	117	10	Q9FKC6	Q9fkc6 arabidopsis
600	4	50.0	117	10	Q9M3N4	Q9m3n4 hordeum vul
601	4	50.0	117	11	Q8BL85	Q8bl85 mus musculu
602	4	50.0	118	16	Q92C20	Q92c20 listeria in
603	4	50.0	119	2	Q9RN88	Q9rn88 salmonella
604	4	50.0	119	10	O48571	O48571 antirrhinum
605	4	50.0	119	16	Q92CI9	Q92ci9 listeria in
606	4	50.0	119	16	Q8NLF5	Q8nlf5 corynebacte
607	4	50.0	119	16	Q7WEL7	Q7wel7 bordetella
608	4	50.0	119	16	Q7W399	Q7w399 bordetella
609	4	50.0	119	16	Q7VU55	Q7vu55 bordetella
610	4	50.0	119	16	Q7VJ39	Q7vj39 helicobacte
611	4	50.0	120	2	Q9LAL3	Q9lal3 moraxella c
612	4	50.0	120	12	Q7TFF9	Q7tff9 rhesus cyto
613	4	50.0	121	8	Q37671	Q37671 schlech tend
614	4	50.0	121	13	Q800I7	Q800i7 oryzias lat
615	4	50.0	121	17	O27846	O27846 methanobact
616	4	50.0	122	16	Q87WB4	Q87wb4 pseudomonas
617	4	50.0	123	5	Q9VMH6	Q9vmh6 drosophila
618	4	50.0	123	5	Q9N8P9	Q9n8p9 trypanosoma
619	4	50.0	123	9	Q9G043	Q9g043 bacterioph
620	4	50.0	123	10	Q7XXI4	Q7xxi4 oryza sativ
621	4	50.0	124	16	Q9AA35	Q9aa35 caulobacter
622	4	50.0	124	16	Q8EAU5	Q8eau5 shewanella
623	4	50.0	124	16	Q7WKI1	Q7wki1 bordetella
624	4	50.0	124	16	Q7W936	Q7w936 bordetella
625	4	50.0	124	16	Q7VY79	Q7vy79 bordetella
626	4	50.0	124	16	Q7UKV7	Q7ukv7 rhodopirell
627	4	50.0	125	2	Q9RCJ4	Q9rcj4 streptococc

628	4	50.0	125	12	Q9J0E5	Q9j0e5 tick-borne
629	4	50.0	125	16	Q9HV13	Q9hvl3 pseudomonas
630	4	50.0	125	16	Q9CHE8	Q9che8 lactococcus
631	4	50.0	125	16	Q8YW04	Q8yw04 anabaena sp
632	4	50.0	125	16	Q8NMI8	Q8nmi8 corynebacte
633	4	50.0	126	16	Q8DIY5	Q8diy5 synechococc
634	4	50.0	126	16	Q8D9C5	Q8d9c5 vibrio vuln
635	4	50.0	127	8	Q9MIB0	Q9mib0 schistosoma
636	4	50.0	128	16	Q9KMM0	Q9kmm0 vibrio chol
637	4	50.0	128	17	Q9HLU0	Q9hlu0 thermoplasm
638	4	50.0	129	2	Q9S3I8	Q9s3i8 haemophilus
639	4	50.0	129	2	O32626	O32626 haemophilus
640	4	50.0	129	5	Q9N8P8	Q9n8p8 trypanosoma
641	4	50.0	129	12	Q89674	Q89674 turkey herp
642	4	50.0	129	12	Q80IV5	Q80iv5 human adeno
643	4	50.0	129	12	Q9DPP6	Q9dpp6 meleagrid h
644	4	50.0	130	9	Q94M43	Q94m43 streptococc
645	4	50.0	130	10	Q8L894	Q8l894 cicer ariet
646	4	50.0	130	10	Q84Z83	Q84z83 oryza sativ
647	4	50.0	130	17	Q9HS36	Q9hs36 halobacteri
648	4	50.0	131	3	Q871B4	Q871b4 neurospora
649	4	50.0	131	5	Q8I8R9	Q8i8r9 anopheles g
650	4	50.0	131	16	Q8XX67	Q8xx67 ralstonia s
651	4	50.0	131	16	Q8XFZ2	Q8xfz2 salmonella
652	4	50.0	131	17	Q8TUP9	Q8tup9 methanosarc
653	4	50.0	132	3	Q9P6S6	Q9p6s6 schizosacch
654	4	50.0	132	3	P78948	P78948 schizosacch
655	4	50.0	132	16	Q8DKW9	Q8dkw9 synechococc
656	4	50.0	133	2	Q47121	Q47121 escherichia
657	4	50.0	133	10	Q7XY30	Q7xy30 griffithsia
658	4	50.0	133	12	Q9DVZ8	Q9dvz8 plutella xy
659	4	50.0	133	12	O39438	O39438 rabies viru
660	4	50.0	133	12	O41853	O41853 duvenhage v
661	4	50.0	133	16	Q98IY9	Q98iy9 rhizobium l
662	4	50.0	133	16	O07321	O07321 staphylococ
663	4	50.0	133	16	Q8CPK9	Q8cpk9 staphylococ
664	4	50.0	133	16	Q87GA4	Q87ga4 vibrio para
665	4	50.0	134	10	Q8H517	Q8h517 oryza sativ
666	4	50.0	134	12	Q991M4	Q991m4 cetacean mo
667	4	50.0	134	16	Q88DT9	Q88dt9 pseudomonas
668	4	50.0	135	12	Q8QPB9	Q8qpb9 duvenhage v
669	4	50.0	135	12	Q8QPC0	Q8qpc0 duvenhage v
670	4	50.0	135	12	Q8QPC1	Q8qpcl duvenhage v
671	4	50.0	135	16	Q9PFX0	Q9pfx0 xylella fas
672	4	50.0	136	5	Q8MQ89	Q8mq89 caenorhabdi
673	4	50.0	136	16	Q92PX3	Q92px3 rhizobium m
674	4	50.0	136	17	O28314	O28314 archaeoglob
675	4	50.0	137	12	Q9IZF1	Q9izf1 tick-borne
676	4	50.0	137	12	Q91E36	Q91e36 phocid herp
677	4	50.0	137	12	Q83000	Q83000 bunyavirus
678	4	50.0	138	2	Q9XDG5	Q9xdg5 escherichia
679	4	50.0	138	4	Q9NSN2	Q9nsn2 homo sapien
680	4	50.0	138	8	Q9MH42	Q9mh42 peperomia a
681	4	50.0	138	9	Q8W6Z9	Q8w6z9 cyanophage
682	4	50.0	138	10	Q9ZRD7	Q9zrd7 glycine max
683	4	50.0	138	12	Q7TAD9	Q7tad9 human enter
684	4	50.0	138	12	Q7TAD8	Q7tad8 human enter

685	4	50.0	138	12	Q7TAD7	Q7tad7 human enter
686	4	50.0	138	12	Q7TAD6	Q7tad6 human enter
687	4	50.0	138	12	Q7TAD5	Q7tad5 human enter
688	4	50.0	138	12	Q7TAD4	Q7tad4 human enter
689	4	50.0	138	12	Q7TAD3	Q7tad3 human enter
690	4	50.0	138	12	Q7TAD2	Q7tad2 human enter
691	4	50.0	138	12	Q7TAD1	Q7tad1 human enter
692	4	50.0	138	12	Q7TAC9	Q7tac9 human enter
693	4	50.0	138	12	Q7TAC8	Q7tac8 human enter
694	4	50.0	138	12	Q7TAC5	Q7tac5 human enter
695	4	50.0	138	12	Q7TAC4	Q7tac4 human enter
696	4	50.0	138	12	Q7TAC3	Q7tac3 human enter
697	4	50.0	138	12	Q7TAC2	Q7tac2 human enter
698	4	50.0	138	12	Q7TAC1	Q7tac1 human enter
699	4	50.0	138	12	Q7TAC0	Q7tac0 human enter
700	4	50.0	138	12	Q7TAB9	Q7tab9 human enter
701	4	50.0	138	12	Q7TAB7	Q7tab7 human enter
702	4	50.0	138	12	Q7TAB6	Q7tab6 human enter
703	4	50.0	138	12	Q7TA98	Q7ta98 human enter
704	4	50.0	138	16	Q8UE72	Q8ue72 agrobacteri
705	4	50.0	138	16	Q81TH2	Q81th2 bacillus an
706	4	50.0	138	16	Q81GB5	Q81gb5 bacillus ce
707	4	50.0	139	2	Q9RCH8	Q9rch8 azotobacter
708	4	50.0	139	9	Q855M1	Q855ml mycobacteri
709	4	50.0	139	10	Q941G0	Q941g0 theobroma c
710	4	50.0	139	10	Q941G1	Q941g1 theobroma c
711	4	50.0	139	10	Q941G2	Q941g2 theobroma c
712	4	50.0	139	10	Q941F9	Q941f9 theobroma c
713	4	50.0	139	17	Q8TPP3	Q8tpp3 methanosarc
714	4	50.0	140	10	Q9FWM1	Q9fwm1 oryza sativ
715	4	50.0	140	10	Q7XDJ8	Q7xdj8 oryza sativ
716	4	50.0	141	12	Q91GF6	Q91gf6 epiphyas po
717	4	50.0	141	16	Q92D32	Q92d32 listeria in
718	4	50.0	141	16	Q8Y8B9	Q8y8b9 listeria mo
719	4	50.0	141	16	Q8ERS2	Q8ers2 oceanobacil
720	4	50.0	141	16	Q8CXS0	Q8cxs0 leptospira
721	4	50.0	141	17	Q8PX95	Q8px95 methanosarc
722	4	50.0	142	2	Q8RQK1	Q8rqk1 bacillus ce
723	4	50.0	142	5	O16896	O16896 caenorhabdi
724	4	50.0	142	12	Q9IZ44	Q9iz44 tick-borne
725	4	50.0	142	16	Q9K7K4	Q9k7k4 bacillus ha
726	4	50.0	142	16	Q9A6Q4	Q9a6q4 caulobacter
727	4	50.0	143	4	Q9H935	Q9h935 homo sapien
728	4	50.0	143	5	Q25610	Q25610 onchocerca
729	4	50.0	143	9	Q853S0	Q853s0 mycobacteri
730	4	50.0	143	16	Q9CEL1	Q9cell1 lactococcus
731	4	50.0	143	16	Q836M6	Q836m6 enterococcu
732	4	50.0	144	10	Q9ZWM1	Q9zwm1 raphanus sa
733	4	50.0	144	16	Q97NG2	Q97ng2 streptococc
734	4	50.0	144	16	Q8FEK0	Q8fek0 escherichia
735	4	50.0	144	16	Q8DN75	Q8dn75 streptococc
736	4	50.0	145	10	O23823	O23823 nicotiana t
737	4	50.0	145	10	Q852T8	Q852t8 brassica ju
738	4	50.0	145	12	Q91MX8	Q91mx8 lumpy skin
739	4	50.0	145	12	Q8JTW9	Q8jtw9 lumpy skin
740	4	50.0	145	16	Q8KE98	Q8ke98 chlorobium
741	4	50.0	145	16	Q82ID9	Q82id9 streptomyce



742	4	50.0	145	17	Q9V2N3	Q9v2n3 pyrococcus
743	4	50.0	146	1	Q9C4S4	Q9c4s4 halobacteri
744	4	50.0	146	2	Q7WX31	Q7wx31 alcaligenes
745	4	50.0	146	5	Q9XUA6	Q9xua6 caenorhabdi
746	4	50.0	146	5	Q26260	Q26260 onchocerca
747	4	50.0	146	8	Q36135	Q36135 tuberaphis
748	4	50.0	146	12	Q7TAB8	Q7tab8 human enter
749	4	50.0	146	16	Q8F4T6	Q8f4t6 leptospira
750	4	50.0	146	17	Q96X70	Q96x70 sulfolobus
751	4	50.0	147	2	Q9RNE9	Q9rne9 escherichia
752	4	50.0	147	2	Q8KK65	Q8kk65 proteus vul
753	4	50.0	147	10	Q9SXT9	Q9sxt9 cicer ariet
754	4	50.0	147	10	Q7XIA0	Q7xia0 oryza sativ
755	4	50.0	147	15	Q8QFJ4	Q8qfj4 chimpanzee
756	4	50.0	147	16	P74066	P74066 synechocyst
757	4	50.0	147	16	Q8E7L4	Q8e7l4 streptococc
758	4	50.0	147	16	Q8E254	Q8e254 streptococc
759	4	50.0	147	16	Q81YF3	Q81yf3 bacillus an
760	4	50.0	148	6	Q862Y7	Q862y7 bos taurus
761	4	50.0	148	10	Q7XLG5	Q7xlg5 oryza sativ
762	4	50.0	148	11	Q9CXA5	Q9cxa5 mus musculu
763	4	50.0	148	12	Q9WIJ2	Q9wij2 human enter
764	4	50.0	148	12	Q9WIJ3	Q9wij3 human enter
765	4	50.0	148	15	Q8QFJ1	Q8qfj1 chimpanzee
766	4	50.0	148	15	Q8QFJ9	Q8qfj9 human immun
767	4	50.0	148	15	Q8QFJ3	Q8qfj3 chimpanzee
768	4	50.0	148	15	Q8QFJ2	Q8qfj2 chimpanzee
769	4	50.0	148	15	Q8QFK0	Q8qfk0 human immun
770	4	50.0	148	16	Q986Z7	Q986z7 rhizobium l
771	4	50.0	148	16	Q8Y906	Q8y906 listeria mo
772	4	50.0	149	10	Q9LF57	Q9lf57 arabidopsis
773	4	50.0	149	10	Q9FXK6	Q9fxk6 arabidopsis
774	4	50.0	149	12	Q81056	Q81056 human papil
775	4	50.0	149	12	Q81057	Q81057 human papil
776	4	50.0	149	12	Q81058	Q81058 human papil
777	4	50.0	149	12	Q81054	Q81054 human papil
778	4	50.0	149	12	Q81055	Q81055 human papil
779	4	50.0	149	12	Q81059	Q81059 human papil
780	4	50.0	149	16	Q927T1	Q927t1 listeria mo
781	4	50.0	149	16	Q8RH25	Q8rh25 fusobacteri
782	4	50.0	149	16	Q8CM93	Q8cm93 streptococc
783	4	50.0	150	5	Q8MPI2	Q8mpi2 patella vul
784	4	50.0	150	10	Q8LJT7	Q8ljt7 striga herm
785	4	50.0	150	10	Q9SL65	Q9sl65 arabidopsis
786	4	50.0	150	10	Q7XQJ9	Q7xqj9 oryza sativ
787	4	50.0	150	11	Q9Z0X0	Q9z0x0 mus musculu
788	4	50.0	150	11	Q9QZT9	Q9qzt9 mus musculu
789	4	50.0	150	12	Q8UYI9	Q8uyi9 swinepox vi
790	4	50.0	150	16	Q8YXB5	Q8yxb5 anabaena sp
791	4	50.0	151	4	Q8N8Z4	Q8n8z4 homo sapien
792	4	50.0	151	5	O77003	O77003 biophalari
793	4	50.0	151	5	Q9U0U4	Q9u0u4 leishmania
794	4	50.0	151	10	Q8LJL3	Q8ljl3 oryza sativ
795	4	50.0	151	10	Q84L62	Q84l62 hordeum vul
796	4	50.0	151	10	Q84L61	Q84l61 hordeum vul
797	4	50.0	151	12	O89810	O89810 epiphyas po
798	4	50.0	151	12	Q7TAC7	Q7tac7 human enter



799	4	50.0	151	13	Q90YS5	Q90ys5 brachydanio
800	4	50.0	151	15	Q8QFK2	Q8qfk2 human immun
801	4	50.0	151	16	Q98E58	Q98e58 rhizobium l
802	4	50.0	151	16	Q8ZBQ4	Q8zbq4 yersinia pe
803	4	50.0	151	16	Q7USR4	Q7usr4 rhodopirell
804	4	50.0	151	17	O27971	O27971 archaeoglob
805	4	50.0	152	2	Q84A39	Q84a39 serratia pr
806	4	50.0	152	5	Q8I557	Q8i557 plasmodium
807	4	50.0	152	7	Q860T5	Q860t5 gallus gall
808	4	50.0	152	8	Q9T8E1	Q9t8e1 varroa unde
809	4	50.0	152	10	Q8LPT8	Q8lpt8 helianthus
810	4	50.0	152	10	O23981	O23981 hordeum vul
811	4	50.0	152	10	Q9C9A3	Q9c9a3 arabidopsis
812	4	50.0	152	10	Q9LZK0	Q9lzk0 arabidopsis
813	4	50.0	152	11	Q9CQW6	Q9cqW6 mus musculu
814	4	50.0	152	12	Q7TAC6	Q7tac6 human enter
815	4	50.0	152	16	Q8UH39	Q8uh39 agrobacteri
816	4	50.0	152	16	Q82FL6	Q82fl6 streptomyce
817	4	50.0	152	17	Q972H6	Q972h6 sulfolobus
818	4	50.0	153	2	Q7WWU5	Q7wwu5 alcaligenes
819	4	50.0	153	6	Q28834	Q28834 oryctolagus
820	4	50.0	153	10	Q9AQY5	Q9aqy5 polytomella
821	4	50.0	153	10	Q9ZW31	Q9zw31 arabidopsis
822	4	50.0	153	10	Q8LGG1	Q8lgg1 arabidopsis
823	4	50.0	153	10	Q9SZN7	Q9szn7 arabidopsis
824	4	50.0	153	10	Q7XY47	Q7xy47 griffithsia
825	4	50.0	153	12	Q9J0E6	Q9j0e6 tick-borne
826	4	50.0	153	16	Q98PQ9	Q98pq9 mycoplasma
827	4	50.0	154	10	Q9M1X5	Q9mlx5 arabidopsis
828	4	50.0	154	11	Q99P99	Q99p99 rattus norv
829	4	50.0	154	12	Q7TAD0	Q7tad0 human enter
830	4	50.0	154	16	Q9JTD4	Q9jtd4 neisseria m
831	4	50.0	154	16	Q8ZF09	Q8zf09 yersinia pe
832	4	50.0	154	16	Q893B9	Q893b9 clostridium
833	4	50.0	154	16	Q81AM1	Q81am1 bacillus ce
834	4	50.0	154	17	O58036	O58036 pyrococcus
835	4	50.0	154	17	Q8ZVW6	Q8zvw6 pyrobaculum
836	4	50.0	155	2	Q93EL9	Q93el9 borrelia bu
837	4	50.0	155	2	Q9JPE9	Q9jpe9 neisseria m
838	4	50.0	155	5	Q8IGE1	Q8igel drosophila
839	4	50.0	155	8	Q85JJ4	Q85jj4 sphaerospir
840	4	50.0	155	10	Q9XIE3	Q9xie3 arabidopsis
841	4	50.0	155	10	Q8LBH7	Q8lbh7 arabidopsis
842	4	50.0	155	11	Q7TML4	Q7tml4 mus musculu
843	4	50.0	155	16	Q9PP27	Q9pp27 campylobact
844	4	50.0	155	16	Q89SD9	Q89sd9 bradyrhizob
845	4	50.0	155	16	Q883M4	Q883m4 pseudomonas
846	4	50.0	155	17	Q9UZ40	Q9uz40 pyrococcus
847	4	50.0	155	17	Q8PSB3	Q8psb3 methanosarc
848	4	50.0	156	2	Q8KY19	Q8kyl9 pseudomonas
849	4	50.0	156	2	Q8KRE2	Q8kre2 pseudomonas
850	4	50.0	156	2	Q9R9C0	Q9r9c0 bacillus th
851	4	50.0	156	2	O30895	O30895 bacillus th
852	4	50.0	156	2	O30969	O30969 bacillus th
853	4	50.0	156	11	Q8K4Y2	Q8k4y2 mus musculu
854	4	50.0	156	11	O88557	O88557 mus musculu
855	4	50.0	156	11	Q8BSN4	Q8bsn4 mus musculu

856	4	50.0	156	16	Q98HV1	Q98hvl rhizobium l
857	4	50.0	156	16	O35016	O35016 bacillus su
858	4	50.0	156	16	Q88QF8	Q88qf8 pseudomonas
859	4	50.0	156	16	Q88EB4	Q88eb4 pseudomonas
860	4	50.0	157	2	O52298	O52298 bacillus th
861	4	50.0	157	8	Q85JG9	Q85jg9 varohadra o
862	4	50.0	157	8	Q85JG8	Q85jg8 varohadra o
863	4	50.0	157	9	Q7Y463	Q7y463 enterobacte
864	4	50.0	157	10	Q8H5C9	Q8h5c9 oryza sativ
865	4	50.0	157	10	Q9LNW0	Q9lnw0 arabidopsis
866	4	50.0	158	4	Q96LQ8	Q96lq8 homo sapien
867	4	50.0	158	5	Q19343	Q19343 caenorhabdi
868	4	50.0	158	5	Q8T751	Q8t751 branchiosto
869	4	50.0	158	8	Q85JJ7	Q85jj7 sphaerospir
870	4	50.0	158	10	Q9SRS0	Q9srs0 arabidopsis
871	4	50.0	158	10	Q8RUZ5	Q8ruz5 arabidopsis
872	4	50.0	159	2	Q9RQD9	Q9rqd9 zymomonas m
873	4	50.0	159	5	Q9U1Y9	Q9uly9 caenorhabdi
874	4	50.0	159	8	Q85JJ9	Q85jj9 sphaerospir
875	4	50.0	159	8	Q85JI2	Q85ji2 sphaerospir
876	4	50.0	159	8	Q85JH5	Q85jh5 sphaerospir
877	4	50.0	159	8	Q85A55	Q85a55 sphaerospir
878	4	50.0	159	16	Q8ZSG0	Q8zsg0 anabaena sp
879	4	50.0	159	16	Q88K77	Q88k77 pseudomonas
880	4	50.0	159	17	O29141	O29141 archaeoglob
881	4	50.0	160	8	Q8WAG4	Q8wag4 hadra belle
882	4	50.0	160	8	Q8WAH0	Q8wah0 hadra belle
883	4	50.0	160	8	Q8W824	Q8w824 hadra belle
884	4	50.0	160	8	Q8WAG9	Q8wag9 hadra belle
885	4	50.0	160	8	Q8WAG7	Q8wag7 hadra belle
886	4	50.0	160	8	Q8W8L1	Q8w8l1 hadra belle
887	4	50.0	160	8	Q8W8S3	Q8w8s3 hadra belle
888	4	50.0	160	8	Q8WAG2	Q8wag2 hadra belle
889	4	50.0	160	8	Q8W7D4	Q8w7d4 hadra belle
890	4	50.0	160	8	Q8W8P5	Q8w8p5 hadra belle
891	4	50.0	160	8	Q8WAG1	Q8wag1 sphaerospir
892	4	50.0	160	8	Q8WAG3	Q8wag3 hadra belle
893	4	50.0	160	8	Q8W8P0	Q8w8p0 hadra belle
894	4	50.0	160	8	Q8W823	Q8w823 hadra belle
895	4	50.0	160	8	Q8WAG6	Q8wag6 hadra belle
896	4	50.0	160	8	Q8WAG5	Q8wag5 hadra belle
897	4	50.0	160	8	Q8WAF7	Q8waf7 sphaerospir
898	4	50.0	160	8	Q8W8P6	Q8w8p6 hadra belle
899	4	50.0	160	8	Q8WAF6	Q8waf6 hadra webbi
900	4	50.0	160	8	Q8WAF8	Q8waf8 sphaerospir
901	4	50.0	160	8	Q85JK1	Q85jk1 camaenid sp
902	4	50.0	160	8	Q85JJ8	Q85jj8 sphaerospir
903	4	50.0	160	8	Q85JJ5	Q85jj5 camaenid sp
904	4	50.0	160	8	Q85JJ2	Q85jj2 sphaerospir
905	4	50.0	160	8	Q85JJ0	Q85jj0 varohadra o
906	4	50.0	160	8	Q85JI8	Q85ji8 sphaerospir
907	4	50.0	160	8	Q85JI7	Q85ji7 sphaerospir
908	4	50.0	160	8	Q85JI6	Q85ji6 sphaerospir
909	4	50.0	160	8	Q85JI5	Q85ji5 sphaerospir
910	4	50.0	160	8	Q85JI4	Q85ji4 sphaerospir
911	4	50.0	160	8	Q85JI3	Q85ji3 sphaerospir
912	4	50.0	160	8	Q85JI1	Q85ji1 sphaerospir

913	4	50.0	160	8	Q85JI0	Q85ji0	sphaerospir
914	4	50.0	160	8	Q85JH9	Q85jh9	sphaerospir
915	4	50.0	160	8	Q85JH8	Q85jh8	sphaerospir
916	4	50.0	160	8	Q85JH7	Q85jh7	sphaerospir
917	4	50.0	160	8	Q85JH6	Q85jh6	sphaerospir
918	4	50.0	160	8	Q85JH4	Q85jh4	sphaerospir
919	4	50.0	160	8	Q85JH3	Q85jh3	sphaerospir
920	4	50.0	160	8	Q85JH2	Q85jh2	sphaerospir
921	4	50.0	160	8	Q85JH0	Q85jh0	varohadra o
922	4	50.0	160	8	Q85CL2	Q85cl2	sphaerospir
923	4	50.0	160	8	Q85CD3	Q85cd3	sphaerospir
924	4	50.0	160	8	Q85AZ1	Q85az1	sphaerospir
925	4	50.0	160	8	Q85AE8	Q85ae8	varohadra o
926	4	50.0	160	8	Q85AE7	Q85ae7	varohadra o
927	4	50.0	160	8	Q859X9	Q859x9	sphaerospir
928	4	50.0	160	10	Q852T7	Q852t7	brassica ju
929	4	50.0	160	10	Q852T5	Q852t5	brassica ju
930	4	50.0	160	10	Q852T4	Q852t4	brassica ju
931	4	50.0	160	11	Q9D0Z5	Q9d0z5	mus musculu
932	4	50.0	160	16	O66445	O66445	aquifex aeo
933	4	50.0	160	16	Q92AD5	Q92ad5	listeria in
934	4	50.0	160	16	Q8Y627	Q8y627	listeria mo
935	4	50.0	160	16	Q8XGZ4	Q8xgz4	ralstonia s
936	4	50.0	160	17	O27749	O27749	methanobact
937	4	50.0	161	5	Q8SWK6	Q8swk6	encephalito
938	4	50.0	161	10	Q8LCS1	Q8lcs1	arabidopsis
939	4	50.0	161	10	Q852T9	Q852t9	brassica ju
940	4	50.0	161	10	Q9LZ38	Q9lz38	arabidopsis
941	4	50.0	161	10	Q7XIU9	Q7xiu9	oryza sativ
942	4	50.0	161	13	Q9DD52	Q9dd52	parexocoetu
943	4	50.0	161	13	Q9DD60	Q9dd60	cypselurus
944	4	50.0	161	16	Q8PNV7	Q8pnv7	xanthomonas
945	4	50.0	161	16	Q8PJK6	Q8pjk6	xanthomonas
946	4	50.0	161	16	Q8PC79	Q8pc79	xanthomonas
947	4	50.0	161	16	Q8P858	Q8p858	xanthomonas
948	4	50.0	161	16	Q7UTB5	Q7utb5	rhodopirell
949	4	50.0	162	5	Q7YZU5	Q7yzu5	eptatretus
950	4	50.0	162	12	Q99BH5	Q99bh5	human cytom
951	4	50.0	162	12	Q99BI6	Q99bi6	human cytom
952	4	50.0	163	4	Q9Y2Y0	Q9y2y0	homo sapien
953	4	50.0	163	5	Q8IQW8	Q8iqw8	drosophila
954	4	50.0	163	10	Q8H210	Q8h210	citrus gran
955	4	50.0	163	11	Q9D385	Q9d385	mus musculu
956	4	50.0	164	2	Q93S78	Q93s78	xanthomonas
957	4	50.0	164	2	Q9RFK2	Q9rfk2	australian
958	4	50.0	164	5	Q9TVN8	Q9tvn8	choristoneu
959	4	50.0	164	5	Q25609	Q25609	onchocerca
960	4	50.0	164	5	Q9TVT8	Q9tvt8	choristoneu
961	4	50.0	164	10	Q8H5C3	Q8h5c3	oryza sativ
962	4	50.0	164	10	O81029	O81029	arabidopsis
963	4	50.0	164	16	Q8NN08	Q8nn08	corynebacte
964	4	50.0	164	16	Q7UBK4	Q7ubk4	shigella fl
965	4	50.0	165	13	Q7SYL1	Q7syll	brachydanio
966	4	50.0	166	5	Q8MUL4	Q8mul4	strongyloce
967	4	50.0	166	10	Q8LEN4	Q8len4	arabidopsis
968	4	50.0	166	10	Q9T038	Q9t038	arabidopsis
969	4	50.0	166	16	Q8XA37	Q8xa37	escherichia

970	4	50.0	166	16	Q8FLA8	Q8fla8 escherichia
971	4	50.0	166	16	Q82U85	Q82u85 nitrosomona
972	4	50.0	167	3	Q9C487	Q9c487 pneumocysti
973	4	50.0	167	5	O45517	O45517 caenorhabdi
974	4	50.0	168	8	Q85QL2	Q85ql2 pachycara b
975	4	50.0	168	8	Q85QL1	Q85ql1 zoarces viv
976	4	50.0	168	10	Q94FC6	Q94fc6 tripsacum d
977	4	50.0	168	10	Q8RW11	Q8rw11 rumex obtus
978	4	50.0	168	16	O68792	O68792 yersinia pe
979	4	50.0	169	4	Q96NP4	Q96np4 homo sapien
980	4	50.0	169	5	Q25611	Q25611 onchocerca
981	4	50.0	169	5	Q7YZA6	Q7yza6 drosophila
982	4	50.0	169	10	Q8GVW5	Q8gvw5 oryza sativ
983	4	50.0	169	12	Q9J0E2	Q9j0e2 tick-borne
984	4	50.0	169	12	Q9IZR6	Q9izr6 tick-borne
985	4	50.0	169	12	Q9IZ43	Q9iz43 tick-borne
986	4	50.0	169	16	Q9K3W8	Q9k3w8 streptomyce
987	4	50.0	169	16	Q82V41	Q82v41 nitrosomona
988	4	50.0	170	2	Q9RQS0	Q9rqs0 escherichia
989	4	50.0	170	2	Q9AH21	Q9ah21 salmonella
990	4	50.0	170	2	Q8KLA2	Q8kla2 rhizobium e
991	4	50.0	170	5	Q86AA0	Q86aa0 dictyosteli
992	4	50.0	170	10	O81055	O81055 arabidopsis
993	4	50.0	170	12	Q9QTE9	Q9qte9 porcine epi
994	4	50.0	170	12	Q9QTE8	Q9qte8 porcine epi
995	4	50.0	170	16	Q89F52	Q89f52 bradyrhizob
996	4	50.0	170	17	O52035	O52035 halobacteri
997	4	50.0	171	2	Q8VP76	Q8vp76 vibrio angu
998	4	50.0	171	5	Q9W1Q0	Q9wlq0 drosophila
999	4	50.0	171	16	Q88F12	Q88f12 pseudomonas
1000	4	50.0	171	16	Q81UM2	Q8lum2 bacillus an

# ALIGNMENTS

## RESULT 1

Q8WZ99

ID Q8WZ99 PRELIMINARY; PRT; 35 AA.

AC Q8WZ99;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Amyloid protein (Fragment).

GN APP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Wakutani Y., Ninomiya H., Iwata H., Tanaka S., Urakami K., Adachi Y.,

RA Wada-Isoe K., Yamagata K., Ohono K., Tsubuki S., Saido T.,

RA Hashimoto T., Iwatsubo T., Nakashima K.;

RT "Novel missense mutation (D678N) of amyloid precursor protein gene in

RT a Japanese pedigree of familial Alzheimer's disease.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB066441; BAB71958.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 35 35  
SQ SEQUENCE 35 AA; 4084 MW; 49D7D17289743B71 CRC64;

Query Match 100.0%; Score 8; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 13 EVKMDAEF 20

#### RESULT 2

O35463

ID O35463 PRELIMINARY; PRT; 79 AA.  
AC O35463;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Alzheimer's amyloid beta protein (Fragment).  
GN BETA APP.  
OS Cricetulus griseus (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10029;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sambamurti K., Pinnix I., Gandhi S.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF030413; AAB86608.1; -.  
DR HSSP; P05067; 1BA4.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
FT NON\_TER 1 1  
FT NON\_TER 79 79  
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 100.0%; Score 8; DB 11; Length 79;  
Best Local Similarity 100.0%; Pred. No. 0.042;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 17 EVKMDAEF 24

#### RESULT 3

Q16020

ID Q16020 PRELIMINARY; PRT; 82 AA.  
AC Q16020;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-amyloid peptide (Fragment).  
 GN BETA APP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor."  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL; S61383; AAB26265.2; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82  
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 8; DB 4; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 14 EVKMDAEF 21

#### RESULT 4

Q16014

ID Q16014 PRELIMINARY; PRT; 82 AA.  
 AC Q16014;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Beta-amyloid peptide (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor."  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 DR EMBL; S60721; AAB26263.2; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 82 82

SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 8; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 14 EVKMDAEF 21

RESULT 5

Q16019

ID Q16019 PRELIMINARY; PRT; 82 AA.  
AC Q16019;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Beta-amyloid peptide (Fragment).  
GN BETA APP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93236601; PubMed=8476439;  
RA Denman R.B., Rosenzwaig R., Miller D.L.;  
RT "A system for studying the effect(s) of familial Alzheimer disease  
RT mutations on the processing of the beta-amyloid peptide precursor."  
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
DR EMBL; S61380; AAB26264.2; -.  
DR HSSP; P05067; 1BA4.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
FT NON\_TER 1 1  
FT NON\_TER 82 82  
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 8; DB 4; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 14 EVKMDAEF 21

RESULT 6

Q8JH58

ID Q8JH58 PRELIMINARY; PRT; 113 AA.  
AC Q8JH58;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Amyloid beta protein (Fragment).



OS Chelydra serpentina serpentina (common snapping turtle).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.  
 OX NCBI\_TaxID=134619;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21876906; PubMed=11882478;  
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;  
 RT "Octylphenol (OP) alters the expression of members of the amyloid  
 RT protein family in the hypothalamus of the snapping turtle, Chelydra  
 RT serpentina serpentina."  
 RL Environ. Health Perspect. 110:269-275(2002).  
 DR EMBL; AF541917; AAN04908.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 8; DB 13; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 0.055;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 11 EVKMDAEF 18

#### RESULT 7

Q8BPV5

ID Q8BPV5 PRELIMINARY; PRT; 218 AA.  
 AC Q8BPV5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Amyloid beta (Fragment).  
 GN APP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK052448; BAC34997.1; -.  
 DR MGD; MGI:88059; App.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR InterPro; IPR008155; A4\_APP.

DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match 100.0%; Score 8; DB 11; Length 218;  
Best Local Similarity 100.0%; Pred. No. 0.093;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 116 EVKMDAEF 123

# RESULT 8

Q8BPC7

ID Q8BPC7 PRELIMINARY; PRT; 384 AA.  
AC Q8BPC7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Amyloid beta (Fragment).  
GN APP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Head;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL; AK076506; BAC36369.1; -.  
DR MGD; MGI:88059; App.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 100.0%; Score 8; DB 11; Length 384;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 282 EVKMDAEF 289

RESULT 9

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.  
 AC O93296;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Amyloid protein (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98337885; PubMed=9671674;  
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,  
 RA Milligan C.E.;  
 RT "Increased production of amyloid precursor protein provides a  
 RT substrate for caspase-3 in dying motoneurons."  
 RL J. Neurosci. 18:5869-5880(1998).  
 DR EMBL; AF042098; AAC25052.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 8; DB 13; Length 534;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 432 EVKMDAEF 439

RESULT 10

Q9PVL1

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.  
 AC Q9PVL1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Amyloid protein (Fragment).  
 GN APP.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;  
 RT "What the evolution of the amyloid protein precursor supergene family  
 RT tells us about its function.";  
 RL Neurochem. Int. 0:0-0(2000).  
 DR EMBL; AF030341; AAF12698.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 100.0%; Score 8; DB 13; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 0.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 468 EVKMDAEF 475

# RESULT 11

Q9DGJ8

ID Q9DGJ8 PRELIMINARY; PRT; 695 AA.  
 AC Q9DGJ8;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Beta-amyloid precursor protein 695 isoform.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sarasa M., Rodolosse A., Sorribas V.;  
 RT "Cloning of full-length chicken beta-amyloid precursor protein  
 RT isoforms.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF289218; AAG00593.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 8; DB 13; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 593 EVKMDAEF 600

# RESULT 12

Q9DGJ7

ID Q9DGJ7 PRELIMINARY; PRT; 751 AA.  
 AC Q9DGJ7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Beta-amyloid precursor protein 751 isoform.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sarasa M., Rodolosse A., Sorribas V.;  
 RT "Cloning of full-length chicken beta-amyloid precursor protein  
 RT isoforms."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF289219; AAG00594.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Protease inhibitor; Serine protease inhibitor.

SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 8; DB 13; Length 751;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
|||||||  
Db 649 EVKMDAEF 656

RESULT 13

Q8IPL5

ID Q8IPL5 PRELIMINARY; PRT; 2148 AA.  
AC Q8IPL5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE CG31652-PA.  
GN CG31652.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phouanenvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AE003608; AAN10513.1; -.  
 DR FlyBase; FBgn0051652; CG31652.  
 DR InterPro; IPR001680; WD40.  
 DR Pfam; PF00400; WD40; 4.  
 DR PROSITE; PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE; PS50294; WD\_REPEATS\_REGION; 1.  
 SQ SEQUENCE 2148 AA; 247689 MW; E3EF2CF71BF3A632 CRC64;

Query Match 87.5%; Score 7; DB 5; Length 2148;  
 Best Local Similarity 100.0%; Pred. No. 8.2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 2 VKMDAEF 8  
 |||||  
Db 1272 VKMDAEF 1278

RESULT 14

Q8IK90

ID Q8IK90 PRELIMINARY; PRT; 254 AA.  
AC Q8IK90;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Proteosome subunit alpha type 1, putative.  
GN PF14\_0716.  
OS Plasmodium falciparum (isolate 3D7).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=36329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3D7;  
RX MEDLINE=22255705; PubMed=12368864;  
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,  
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,  
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,  
RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,  
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,  
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,  
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,  
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,  
RA Fraser C.M., Barrell B.;  
RT "Genome sequence of the human malaria parasite Plasmodium  
RT falciparum.";  
RL Nature 419:498-511(2002).  
DR EMBL; AE014828; AAN37329.1; -.  
DR GO; GO:0005839; C:proteasome core complex (sensu Eukarya); IEA.  
DR GO; GO:0004175; F:endorpeptidase activity; IEA.  
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.  
DR InterPro; IPR001353; Peptidase\_T1.  
DR Pfam; PF00227; proteasome; 1.  
SQ SEQUENCE 254 AA; 28837 MW; 0FCD6C429DDDBB4B CRC64;

Query Match 75.0%; Score 6; DB 5; Length 254;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDAE 7  
 |||||  
Db 235 VKMDAE 240

RESULT 15

Q8A7J6

ID Q8A7J6 PRELIMINARY; PRT; 430 AA.  
AC Q8A7J6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Two-component system sensor histidine kinase.  
 GN BT1528.  
 OS Bacteroides thetaiotaomicron.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=818;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VPI-5482 / ATCC 29148;  
 RX MEDLINE=22550858; PubMed=12663928;  
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
 RA Chiang H.C., Hooper L.V., Gordon J.I.;  
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."  
 RL Science 299:2074-2076(2003).  
 DR EMBL; AE016932; AAO76635.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR003594; ATPbind\_ATPase.  
 DR InterPro; IPR004358; Bact\_sens\_pr\_C.  
 DR InterPro; IPR003660; HAMP.  
 DR InterPro; IPR005467; His\_kinase.  
 DR InterPro; IPR000014; PAS\_domain.  
 DR Pfam; PF00672; HAMP; 1.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR Pfam; PF00989; PAS; 1.  
 DR PRINTS; PR00344; BCTRLSENSOR.  
 DR SMART; SM00304; HAMP; 1.  
 DR SMART; SM00387; HATPase\_c; 1.  
 DR SMART; SM00091; PAS; 1.  
 DR PROSITE; PS50885; HAMP; 1.  
 DR PROSITE; PS50109; HIS\_KIN; 1.  
 DR PROSITE; PS50112; PAS; 1.  
 KW Kinase; Complete proteome.  
 SQ SEQUENCE 430 AA; 48738 MW; 68AC5C1A298C72EF CRC64;

Query Match 75.0%; Score 6; DB 16; Length 430;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDA 6  
 |||||  
 Db 327 EVKMDA 332

# RESULT 16

## Q8N1L0

ID Q8N1L0 PRELIMINARY; PRT; 482 AA.  
 AC Q8N1L0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE cAMP-dependent protein kinase regulatory subunit.  
 GN PKR1.  
 OS Cryptococcus neoformans var. neoformans.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 OX NCBI\_TaxID=40410;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JEC21;  
 RA D'Souza C.A., Cox G.M., Heitman J.;  
 RT "cAMP-dependent protein kinase catalytic subunits have divergent  
 RT functions in different varieties of *Cryptococcus neoformans*."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF481771; AAM74046.1; -.  
 DR GO; GO:0005952; C:cAMP-dependent protein kinase complex; IEA.  
 DR GO; GO:0008603; F:cAMP-dependent protein kinase, intrinsic re. . .; IEA.  
 DR GO; GO:0016301; F:kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR002373; cAMP\_kin.  
 DR InterPro; IPR000595; cNMP\_binding.  
 DR InterPro; IPR003117; RIIa.  
 DR Pfam; PF00027; cNMP\_binding; 2.  
 DR Pfam; PF02197; RIIa; 1.  
 DR PRINTS; PR00103; CAMPKINASE.  
 DR SMART; SM00100; cNMP; 2.  
 DR SMART; SM00394; RIIa; 1.  
 DR PROSITE; PS00888; CNMP\_BINDING\_1; 2.  
 DR PROSITE; PS00889; CNMP\_BINDING\_2; 2.  
 DR PROSITE; PS50042; CNMP\_BINDING\_3; 2.  
 KW Kinase.  
 SQ SEQUENCE 482 AA; 52749 MW; 0F2C20850BA6F044 CRC64;

Query Match 75.0%; Score 6; DB 3; Length 482;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDA 6  
 |||||  
 Db 237 EVKMDA 242

# RESULT 17

Q7WP80

ID Q7WP80 PRELIMINARY; PRT; 637 AA.  
 AC Q7WP80;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN BB0805.  
 OS *Bordetella bronchiseptica* (*Alcaligenes bronchisepticus*).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; *Bordetella*.  
 OX NCBI\_TaxID=518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RB50 / ATCC BAA-588;  
 RX MEDLINE=22827954; PubMed=12910271;  
 RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
 RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,  
 RA Rabbino-witsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 DR EMBL; BX640439; CAE31304.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 637 AA; 70348 MW; EF313925B09803CA CRC64;

Query Match 75.0%; Score 6; DB 16; Length 637;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KMDAEF 8  
 |||||  
 Db 63 KMDAEF 68

# RESULT 18

Q7W1H0

ID Q7W1H0 PRELIMINARY; PRT; 637 AA.  
 AC Q7W1H0;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN BPP0719.  
 OS Bordetella parapertussis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Bordetella.  
 OX NCBI\_TaxID=519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=12822 / ATCC BAA-587;  
 RX MEDLINE=22827954; PubMed=12910271;  
 RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,  
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,  
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,  
 RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,  
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,  
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,  
 RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,  
 RA Rabbino-witsch E., Rutter S., Sanders M., Saunders D., Seeger K.,  
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,  
 RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;  
 RT "Comparative analysis of the genome sequences of Bordetella pertussis,  
 RT Bordetella parapertussis and Bordetella bronchiseptica.";  
 RL Nat. Genet. 35:32-40(2003).  
 DR EMBL; BX640425; CAE40128.1; -.  
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 637 AA; 70294 MW; 6C0315AE6A19DAA7 CRC64;

Query Match 75.0%; Score 6; DB 16; Length 637;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KMDAEF 8  
|||||  
Db 63 KMDAEF 68

RESULT 19

Q898I7

ID Q898I7 PRELIMINARY; PRT; 1080 AA.  
AC Q898I7;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative S-layer protein/N-acetylmuramoyl-L-alanine amidase.  
GN CTC00462.  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Massachusetts / E88;  
RX MEDLINE=22457253; PubMed=12552129;  
RA Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,  
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
RA Gottschalk G.;  
RT "The genome sequence of Clostridium tetani, the causative agent of  
RT tetanus disease.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
DR EMBL; AE015937; AAO35094.1; -.  
DR InterPro; IPR007253; CW\_binding\_2.  
DR Pfam; PF04122; CW\_binding\_2; 2.  
KW Complete proteome.  
SQ SEQUENCE 1080 AA; 118694 MW; C399B0EEEC1C91D4E CRC64;

Query Match 75.0%; Score 6; DB 16; Length 1080;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDAE 7  
|||||  
Db 771 VKMDAE 776

RESULT 20

Q80LR6

ID Q80LR6 PRELIMINARY; PRT; 84 AA.  
AC Q80LR6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.

OS Adoxophyes honmai nucleopolyhedrovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=224399;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ADN001;  
 RA Nakai M., Goto C., Kang W., Shikata M., Kunimi Y.;  
 RT "Sequence and genome organization of a nucleopolyhedrovirus isolated  
 RT from the smaller tea tortrix, Adoxophyes honmai."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AP006270; BAC67281.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 84 AA; 9958 MW; A3487529F7F8F3CF CRC64;

Query Match 62.5%; Score 5; DB 12; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KMDAE 7  
 |||||  
 Db 68 KMDAE 72

#### RESULT 21

Q9X9L6

ID Q9X9L6 PRELIMINARY; PRT; 98 AA.  
 AC Q9X9L6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Putative cytoplasmic protein).  
 GN PSLT025.  
 OS Salmonella typhimurium.  
 OG Plasmid pIP1350, and Plasmid pSLT.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C52; PLASMID=pIP1350;  
 RA Norel F.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720; PLASMID=pSLT;  
 RX MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2."  
 RL Nature 413:852-856(2001).  
 DR EMBL; Y18434; CAB46353.1; -.  
 DR EMBL; AE006471; AAL23525.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Hypothetical protein; Plasmid; Complete proteome.  
SQ SEQUENCE 98 AA; 11311 MW; 5E4E024B0F4B9E94 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8  
|||||  
Db 1 MDAEF 5

#### RESULT 22

##### Q8RFK9

ID Q8RFK9 PRELIMINARY; PRT; 104 AA.  
AC Q8RFK9;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Integral membrane protein.  
GN FN0686.  
OS Fusobacterium nucleatum (subsp. nucleatum).  
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
OC Fusobacterium.  
OX NCBI\_TaxID=76856;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 25586;  
RX MEDLINE=21886394; PubMed=11889109;  
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,  
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,  
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,  
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,  
RA Fonstein M., Kyrpides N., Overbeek R.;  
RT "Genome sequence and analysis of the oral bacterium Fusobacterium  
RT nucleatum strain ATCC 25586."  
RL J. Bacteriol. 184:2005-2018(2002).  
DR EMBL; AE010579; AAL94882.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR005798; Cytb\_b6\_C.  
DR PROSITE; PS00193; CYTOCHROME\_B\_QO; 1.  
KW Complete proteome.  
SQ SEQUENCE 104 AA; 12765 MW; 31F5886974E15881 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMD 5  
|||||  
Db 5 EVKMD 9

#### RESULT 23



Q97XY5

ID Q97XY5 PRELIMINARY; PRT; 127 AA.  
AC Q97XY5;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein SSO1570.  
GN SSO1570.  
OS Sulfolobus solfataricus.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=2287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
RX MEDLINE=21332296; PubMed=11427726;  
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,  
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,  
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,  
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,  
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;  
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
DR EMBL; AE006770; AAK41783.1; -.  
DR PIR; H90315; H90315.  
DR InterPro; IPR007113; Cupin\_sup.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 127 AA; 14710 MW; C358B210A953262F CRC64;

Query Match 62.5%; Score 5; DB 17; Length 127;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
| | | | |  
Db 11 EVKMD 15

RESULT 24

O45467

ID O45467 PRELIMINARY; PRT; 140 AA.  
AC O45467;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE F36D3.10 protein.  
GN F36D3.10.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McMurray A.A.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; Z81531; CAB04323.1; -.  
 DR PIR; T21857; T21857.  
 DR HSSP; P05140; 2AFP.  
 DR WormPep; F36D3.10; CE15974.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 SQ SEQUENCE 140 AA; 15190 MW; 4465EE7064E24934 CRC64;

Query Match 62.5%; Score 5; DB 5; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
 |||||  
 Db 55 KMDAE 59

# RESULT 25

O26386

ID O26386 PRELIMINARY; PRT; 146 AA.  
 AC O26386;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein MTH286.  
 GN MTH286.  
 OS Methanobacterium thermoautotrophicum.  
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
 OC Methanobacteriaceae; Methanothermobacter.  
 OX NCBI\_TaxID=187420;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Delta H;  
 RX MEDLINE=98037514; PubMed=9371463;  
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,  
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,  
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,  
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
 RT deltaH: functional analysis and comparative genomics."  
 RL J. Bacteriol. 179:7135-7155(1997).  
 DR EMBL; AE000814; AAB84792.1; -.  
 DR PIR; C69136; C69136.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 146 AA; 16406 MW; B3F64C92CB941926 CRC64;

Query Match 62.5%; Score 5; DB 17; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 129 EVKMD 133

RESULT 26

Q8SU54

ID Q8SU54 PRELIMINARY; PRT; 147 AA.  
AC Q8SU54;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical protein ECU11\_0740.  
GN ECU11\_0740.  
OS Encephalitozoon cuniculi.  
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.  
OX NCBI\_TaxID=6035;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RA Genoscope;  
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GB-M1;  
RX MEDLINE=21576510; PubMed=11719806;  
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,  
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,  
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,  
RA Weissenbach J., Vivares C.P.;  
RT "Genome sequence and gene compaction of the eukaryote parasite  
RT Encephalitozoon cuniculi.";  
RL Nature 414:450-453(2001).  
DR EMBL; AL590450; CAD25984.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 147 AA; 16314 MW; 503951D6AC1C26EA CRC64;

Query Match 62.5%; Score 5; DB 5; Length 147;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8  
|||||  
Db 4 MDAEF 8

RESULT 27

Q9AU03

ID Q9AU03 PRELIMINARY; PRT; 149 AA.  
AC Q9AU03;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit II (EC 1.9.3.1) (Cytochrome c oxidase  
 DE polypeptide II) (Fragment).  
 GN COX2B.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21179187; PubMed=11094061;  
 RA Perez-Martinez X., Antaramian A., Vazquez-Acevedo M., Funes S.,  
 RA Tolkunova E., d'Alayer J., Claros M.G., Davidson E., King M.P.,  
 RA Gonzalez-Halphen D.;  
 RT "Subunit II of Cytochrome C Oxidase in Chlamydomonad Algae Is a  
 RT Heterodimer Encoded by Two Independent Nuclear Genes.";  
 RL J. Biol. Chem. 276:11302-11309(2001).  
 CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2  
 CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER  
 CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY  
 CC SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME  
 CC C + 2 H(2)O.  
 CC -!- COFACTOR: COPPER A (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
 CC INNER MEMBRANE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
 DR EMBL; AF305540; AAK32114.1; -.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Oxidoreductase;  
 KW Respiratory chain; Transmembrane; Transport; Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 149 AA; 16815 MW; 038CE0375B3415E4 CRC64;

Query Match 62.5%; Score 5; DB 10; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 90 VKMDA 94

RESULT 28

Q9PSV2

ID Q9PSV2 PRELIMINARY; PRT; 150 AA.  
AC Q9PSV2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Ventricular natriuretic peptide.  
OS Anguilla japonica (Japanese eel).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla.  
OX NCBI\_TaxID=7937;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Takei Y.;  
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95200478; PubMed=7893352;  
RA Takei Y., Ueki M., Nishizawa T.;  
RT "Eel ventricular natriuretic peptide: cDNA cloning and mRNA  
RT expression.";  
RL J. Mol. Endocrinol. 13:339-345(1994).  
DR EMBL; AB019371; BAA34121.1; -.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR000663; Natr\_peptide.  
DR Pfam; PF00212; ANP; 1.  
DR PRINTS; PR00710; NATPEPTIDES.  
DR SMART; SM00183; NAT\_PEP; 1.  
DR PROSITE; PS00263; NATRIURETIC\_PEPTIDE; 1.  
SQ SEQUENCE 150 AA; 16735 MW; 919A097362C42519 CRC64;

Query Match 62.5%; Score 5; DB 13; Length 150;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 64 KMDAE 68

RESULT 29

Q9AYR9

ID Q9AYR9 PRELIMINARY; PRT; 153 AA.  
AC Q9AYR9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cytochrome c oxidase subunit 2 (EC 1.9.3.1) (Cytochrome c oxidase  
 DE polypeptide II) (Fragment).  
 GN COX2.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Watanabe K.I., Megumi E., Ohama T.;  
 RT "Evidence of invasive spliceosomal introns in Chlamydomonas  
 RT reinhardtii: introns in recently translocated cox2 and cox3 genes from  
 RT mitochondria to nuclear genome."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2  
 CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER  
 CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY  
 CC SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME  
 CC C + 2 H(2)O.  
 CC -!- COFACTOR: COPPER A (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
 CC INNER MEMBRANE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
 DR EMBL; AB046572; BAB21507.1; -.  
 DR GO; GO:0019866; C:inner membrane; IEA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Oxidoreductase;  
 KW Respiratory chain; Transmembrane; Transport; Mitochondrion.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 153 AA; 17318 MW; F1551FDA60975119 CRC64;

Query Match 62.5%; Score 5; DB 10; Length 153;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30

Q9AU02

ID Q9AU02 PRELIMINARY; PRT; 153 AA.  
AC Q9AU02;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit II (EC 1.9.3.1) (Cytochrome c oxidase  
DE polypeptide II).  
GN COX2B.  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21179187; PubMed=11094061;  
RA Perez-Martinez X., Antaramian A., Vazquez-Acevedo M., Funes S.,  
RA Tolkunova E., d'Alayer J., Claros M.G., Davidson E., King M.P.,  
RA Gonzalez-Halphen D.;  
RT "Subunit II of Cytochrome C Oxidase in Chlamydomonad Algae Is a  
RT Heterodimer Encoded by Two Independent Nuclear Genes."  
RL J. Biol. Chem. 276:11302-11309(2001).  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2  
CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER  
CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY  
CC SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME  
CC C + 2 H(2)O.  
CC -!- COFACTOR: COPPER A (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
CC INNER MEMBRANE (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
DR EMBL; AF305543; AAK32117.1; -.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.  
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001505; Copper\_CuA.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
DR Pfam; PF00116; COX2; 1.



DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Oxidoreductase;  
 KW Respiratory chain; Transmembrane; Transport; Mitochondrion.  
 SQ SEQUENCE 153 AA; 17250 MW; 616BCD26B26A7EC8 CRC64;

Query Match 62.5%; Score 5; DB 10; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 94 VKMDA 98

# RESULT 31

Q92VL2

ID Q92VL2 PRELIMINARY; PRT; 153 AA.  
 AC Q92VL2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Putative MaoC-like (Monoamine oxidase-like) protein, similar to NodN  
 DE (EC 1.4.3.4).  
 GN RB0689 OR SMB21110.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OG Plasmid pSymB (megaplasmid 2).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396508; PubMed=11481431;  
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,  
 RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,  
 RA Golding B., Puehler A.;  
 RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-  
 RT fixing endosymbiont Sinorhizobium meliloti.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).  
 DR EMBL; AL603644; CAC49089.1; -.  
 DR PIR; A95928; A95928.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 DR GO; GO:0004041; F:amine oxidase (flavin-containing) activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002539; MaoC\_dehydratas.  
 DR Pfam; PF01575; MaoC\_dehydratas; 1.  
 KW Oxidoreductase; Plasmid; Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 153 AA; 17044 MW; 85741F8CE696D405 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8

Db                   |||||  
                    44 MDAEF 48

RESULT 32

Q8H004

ID   Q8H004           PRELIMINARY;           PRT;   155 AA.  
AC   Q8H004;  
DT   01-MAR-2003 (TrEMBLrel. 23, Created)  
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE   Hypothetical protein.  
GN   OJ1081D05.12.  
OS   Oryza sativa (japonica cultivar-group).  
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC   Ehrhartoideae; Oryzeae; Oryza.  
OX   NCBI\_TaxID=39947;  
RN   [1]  
RP   SEQUENCE FROM N.A.  
RA   Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,  
RA   Collura K.;  
RT   "Rice Genomic Sequence."  
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
DR   EMBL; AC134229; AAO06978.1; -.  
KW   Hypothetical protein.  
SQ   SEQUENCE   155 AA; 16921 MW; 6602CA80E32B5006 CRC64;

Query Match                   62.5%;   Score 5;   DB 10;   Length 155;  
Best Local Similarity   100.0%;   Pred. No. 2.1e+02;  
Matches       5;   Conservative       0;   Mismatches       0;   Indels       0;   Gaps       0;

Qy                   4 MDAEF 8  
                    |||||  
Db                   141 MDAEF 145

RESULT 33

Q896C5

ID   Q896C5           PRELIMINARY;           PRT;   155 AA.  
AC   Q896C5;  
DT   01-JUN-2003 (TrEMBLrel. 24, Created)  
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE   Hypothetical protein.  
GN   CTC01083.  
OS   Clostridium tetani.  
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC   Clostridium.  
OX   NCBI\_TaxID=1513;  
RN   [1]  
RP   SEQUENCE FROM N.A.  
RC   STRAIN=Massachusetts / E88;  
RX   MEDLINE=22457253; PubMed=12552129;  
RA   Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,  
RA   Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,  
RA   Gottschalk G.;

RT "The genome sequence of Clostridium tetani, the causative agent of  
 RT tetanus disease."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).  
 DR EMBL; AE015939; AAO35665.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 155 AA; 18503 MW; 34198AA82700080F CRC64;

Query Match 62.5%; Score 5; DB 16; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
 |||||  
 Db 128 EVKMD 132

# RESULT 34

Q8TX53

ID Q8TX53 PRELIMINARY; PRT; 163 AA.  
 AC Q8TX53;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Transcription antiterminator NusG.  
 GN NUSG OR MK0823.  
 OS Methanopyrus kandleri.  
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
 OC Methanopyrus.  
 OX NCBI\_TaxID=2320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
 RX MEDLINE=21927647; PubMed=11930014;  
 RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,  
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
 RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
 RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;  
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19  
 RT and monophyly of archaeal methanogens."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
 DR EMBL; AE010373; AAM02036.1; -.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:0003711; F:transcriptional elongation regulator activity; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR003257; Bac\_NusG.  
 DR InterPro; IPR005824; KOW.  
 DR InterPro; IPR006646; KOW\_sub.  
 DR InterPro; IPR006645; NgN.  
 DR InterPro; IPR005825; Ribosomal\_L24\_26.  
 DR InterPro; IPR008991; Transl\_SH3\_like.  
 DR Pfam; PF00467; KOW; 1.  
 DR ProDom; PD005267; Bac\_NusG; 1.  
 DR SMART; SM00739; KOW; 1.  
 DR SMART; SM00738; NGN; 1.

DR TIGRFAMs; TIGR00405; L26e\_arch; 1.  
DR PROSITE; PS01108; RIBOSOMAL\_L24; 1.  
KW Complete proteome.  
SQ SEQUENCE 163 AA; 18419 MW; D22FF483F7EB9DB7 CRC64;

Query Match 62.5%; Score 5; DB 17; Length 163;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 148 VKMDA 152

RESULT 35

Q9B2F3

ID Q9B2F3 PRELIMINARY; PRT; 174 AA.  
AC Q9B2F3;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit II (EC 1.9.3.1) (Cytochrome c oxidase  
DE polypeptide II) (Fragment).  
GN COII.  
OS Beroe ovata.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Ctenophora; Cyclocoela; Beroida; Beroidae; Beroe.  
OX NCBI\_TaxID=10201;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Watkins R.F., Beckenbach A.T.;  
RT "The rate of sequence evolution in mitochondrial genes of the  
RT Demospongiae, Calcispongiae, and Anthozoa is very low relative to the  
RT bilateral animals."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2  
CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER  
CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY  
CC SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME  
CC C + 2 H(2)O.  
CC -!- COFACTOR: COPPER A (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
CC INNER MEMBRANE (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
DR EMBL; AF362019; AAK27370.1; -.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.

DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 KW Copper; Electron transport; Inner membrane; Membrane; Oxidoreductase;  
 KW Respiratory chain; Transmembrane; Transport; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 174 174  
 SQ SEQUENCE 174 AA; 19753 MW; 1748A52F36E39938 CRC64;

Query Match 62.5%; Score 5; DB 8; Length 174;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 162 VKMDA 166

#### RESULT 36

Q847P4

ID Q847P4 PRELIMINARY; PRT; 175 AA.  
 AC Q847P4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Rp L6 (Fragment).  
 OS Aster yellows phytoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Phytoplasma.  
 OX NCBI\_TaxID=35779;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Melamed S., Tanne E., Ben-Haim R., Edelbaum O., Yogev D., Sela I.;  
 RT "A Novel Approach to the Study of the Phytoplasma Genome and the  
 RT Characterization of Sixty Phytoplasmal Genes."  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY191298; AAO61992.1; -.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR000702; Ribosomal\_L6.  
 DR InterPro; IPR002358; Ribosomal\_L6\_1.  
 DR Pfam; PF00347; Ribosomal\_L6; 2.  
 DR PRINTS; PR00059; RIBOSOMALL6.  
 DR ProDom; PD002236; Ribosomal\_L6; 1.  
 DR PROSITE; PS00525; RIBOSOMAL\_L6\_1; 1.  
 FT NON\_TER 175 175  
 SQ SEQUENCE 175 AA; 20012 MW; 5B3BB77EF6735CFF CRC64;

Query Match 62.5%; Score 5; DB 2; Length 175;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 135 EVKMD 139

RESULT 37

Q97NQ1

ID Q97NQ1 PRELIMINARY; PRT; 179 AA.  
AC Q97NQ1;  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Type II DNA modification methyltransferase, putative.  
GN SP1969.  
OS Streptococcus pneumoniae.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1313;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC BAA-334 / TIGR4;  
RX MEDLINE=21357209; PubMed=11463916;  
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,  
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,  
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,  
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,  
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,  
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,  
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,  
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;  
RT "Complete genome sequence of a virulent isolate of Streptococcus  
RT pneumoniae.";  
RL Science 293:498-506(2001).  
DR EMBL; AE007487; AAK76036.1; -.  
DR PIR; C95230; C95230.  
DR TIGR; SP1969; -.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.  
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006306; P:DNA methylation; IEA.  
DR InterPro; IPR004398; Cons\_hypoth95.  
DR InterPro; IPR002052; N6\_Mtase.  
DR InterPro; IPR000051; SAM\_bind.  
DR Pfam; PF03602; Cons\_hypoth95; 1.  
DR TIGRFAMs; TIGR00095; TIGR00095; 1.  
DR PROSITE; PS00092; N6\_MTASE; 1.  
KW Transferase; Methyltransferase; Complete proteome.  
SQ SEQUENCE 179 AA; 19886 MW; 06DD5874D839A349 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 179;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 97 KMDAE 101

RESULT 38

Q8DNE5

ID Q8DNE5 PRELIMINARY; PRT; 179 AA.  
AC Q8DNE5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Conserved hypothetical protein.  
GN SPR1784.  
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=171101;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21429245; PubMed=11544234;  
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,  
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,  
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,  
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,  
RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,  
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,  
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,  
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,  
RA Glass J.I.;  
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";  
RL J. Bacteriol. 183:5709-5717(2001).  
DR EMBL; AE008543; AAL00587.1; -.  
DR PIR; F98094; F98094.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.  
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.  
DR GO; GO:0006306; P:DNA methylation; IEA.  
DR InterPro; IPR004398; Cons\_hypoth95.  
DR InterPro; IPR002052; N6\_Mtase.  
DR InterPro; IPR000051; SAM\_bind.  
DR Pfam; PF03602; Cons\_hypoth95; 1.  
DR TIGRFAMs; TIGR00095; TIGR00095; 1.  
DR PROSITE; PS00092; N6\_MTASE; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 179 AA; 19843 MW; B0042111CD34CEEA CRC64;

Query Match 62.5%; Score 5; DB 16; Length 179;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
|||||  
Db 97 KMDAE 101



RESULT 39

Q9B2F6

ID Q9B2F6 PRELIMINARY; PRT; 184 AA.  
AC Q9B2F6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit II (EC 1.9.3.1) (Cytochrome c oxidase  
DE polypeptide II) (Fragment).  
GN COII.  
OS Halichondria sp. RFW-2001.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;  
OC Halichondrida; Halichondriidae; Halichondria.  
OX NCBI\_TaxID=155678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Watkins R.F., Beckenbach A.T.;  
RT "The rate of sequence evolution in mitochondrial genes of the  
RT Demospongiae, Calcispongiae, and Anthozoa is very low relative to the  
RT bilateral animals.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-  
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2  
CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER  
CC A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY  
CC SIMILARITY).  
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME  
CC C + 2 H(2)O.  
CC -!- COFACTOR: COPPER A (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL  
CC INNER MEMBRANE (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.  
DR EMBL; AF362016; AAK27367.1; -.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0009481; F:aa3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009482; F:ba3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009483; F:caa3-type cytochrome c oxidase; IEA.  
DR GO; GO:0009485; F:cbb3-type cytochrome c oxidase; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.  
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001505; Copper\_CuA.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
DR Pfam; PF00116; COX2; 1.  
DR Pfam; PF02790; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXIDASEII.  
DR ProDom; PD000131; Copper\_CuA; 1.  
KW Copper; Electron transport; Inner membrane; Membrane; Oxidoreductase;

KW Respiratory chain; Transmembrane; Transport; Mitochondrion.  
FT NON\_TER 1 1  
FT NON\_TER 184 184  
SQ SEQUENCE 184 AA; 21292 MW; 03257B258FB8AA4F CRC64;

Query Match 62.5%; Score 5; DB 8; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 156 VKMDA 160

RESULT 40

Q82W02

ID Q82W02 PRELIMINARY; PRT; 185 AA.  
AC Q82W02;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Elongation factor P (EF-P).  
GN EFP OR NE0897.  
OS Nitrosomonas europaea.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
OC Nitrosomonadaceae; Nitrosomonas.  
OX NCBI\_TaxID=915;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19718 / IFO 14298;  
RX MEDLINE=22586410; PubMed=12700255;  
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,  
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,  
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;  
RT "Complete genome sequence of the ammonia-oxidizing bacterium and  
RT obligate chemolithoautotroph Nitrosomonas europaea."  
RL J. Bacteriol. 185:2759-2773(2003).  
DR EMBL; BX321859; CAD84808.1; -.  
DR GO; GO:0003746; F:translation elongation factor activity; IEA.  
DR GO; GO:0006414; P:translational elongation; IEA.  
DR InterPro; IPR001059; EF-P.  
DR Pfam; PF01132; EFP; 1.  
DR TIGRFAMs; TIGR00038; efp; 1.  
KW Elongation factor; Complete proteome.  
SQ SEQUENCE 185 AA; 21071 MW; A023AF94E252A375 CRC64;

Query Match 62.5%; Score 5; DB 16; Length 185;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8  
|||||  
Db 83 MDAEF 87

Search completed: March 26, 2004, 15:35:00  
Job time : 70 secs

OM protein - protein search, using sw model

Run on: March 26, 2004, 15:30:32 ; Search time 10.5 Seconds  
 (without alignments)  
 39.672 Million cell updates/sec

Title: US-09-668-314C-70  
 Perfect score: 8  
 Sequence: 1 EVKMDAEF 8

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	8	100.0	57	1	A4_URSMA	Q29149 ursus marit
2	8	100.0	58	1	A4_CANFA	Q28280 canis famil
3	8	100.0	58	1	A4_RABIT	Q28748 oryctolagus
4	8	100.0	58	1	A4_SHEEP	Q28757 ovis aries
5	8	100.0	59	1	A4_BOVIN	Q28053 bos taurus
6	8	100.0	751	1	A4_SAISC	Q95241 s amyloid b
7	8	100.0	770	1	A4_CAVPO	Q60495 c amyloid b
8	8	100.0	770	1	A4_HUMAN	P05067 h amyloid b
9	8	100.0	770	1	A4_MACFA	P53601 m amyloid b
10	8	100.0	770	1	A4_MOUSE	P12023 m amyloid b
11	8	100.0	770	1	A4_PIG	P79307 s amyloid b
12	8	100.0	770	1	A4_RAT	P08592 r amyloid b
13	6	75.0	656	1	V091_FOWPV	072896 fowlpox vir
14	5	62.5	82	1	U222_DROME	Q8mqi6 drosophila
15	5	62.5	82	1	U222_MANSE	Q9u501 manduca sex
16	5	62.5	84	1	U222_CAEEL	Q9xvz8 caenorhabdi
17	5	62.5	168	1	YF24_MYCPN	P75254 mycoplasma

18	5	62.5	196	1	YF01_MYCPN	P75286	mycoplasma
19	5	62.5	217	1	BIOS_RHIME	O08250	rhizobium m
20	5	62.5	218	1	HRF1_NPVLD	Q90165	lymantria d
21	5	62.5	224	1	COX2_ALBCO	P48889	albinaria c
22	5	62.5	224	1	COX2_ALBTU	Q09334	albinaria t
23	5	62.5	229	1	COX2_PARLI	P12701	paracentrot
24	5	62.5	230	1	COX2_CARAU	O78682	carassius a
25	5	62.5	230	1	COX2_CROLA	P34189	crossostoma
26	5	62.5	230	1	COX2_CYPCA	P24987	cyprinus ca
27	5	62.5	230	1	COX2_ONCMY	P48171	oncorhynchu
28	5	62.5	230	1	COX2_SALSA	Q37677	salmo salar
29	5	62.5	230	1	COX2_SCYCA	O79404	scyliorhinu
30	5	62.5	230	1	COX2_SQUAC	Q9zz51	squalus aca
31	5	62.5	231	1	COX2_LATCH	O03848	latimeria c
32	5	62.5	233	1	RSUA_VIBVU	Q8d8x2	vibrio vuln
33	5	62.5	247	1	CD8A_MOUSE	P01731	mus musculu
34	5	62.5	248	1	COX2_METSE	O47496	metridium s
35	5	62.5	269	1	T2S1_STRFI	O52512	streptomyce
36	5	62.5	276	1	SACT_BACSU	P26212	bacillus su
37	5	62.5	284	1	FLAL_VIBPA	Q03473	vibrio para
38	5	62.5	371	1	VINT_BPML5	P22884	mycobacteri
39	5	62.5	414	1	K193_HUMAN	Q12765	homo sapien
40	5	62.5	419	1	DCDA_ARCFU	O29458	archaeoglob
41	5	62.5	452	1	F26_YEAST	P32604	saccharomyc
42	5	62.5	457	1	CD4_RAT	P05540	rattus norv
43	5	62.5	461	1	MYH_SCHPO	Q10159	schizosacch
44	5	62.5	461	1	NCB1_HUMAN	Q02818	homo sapien
45	5	62.5	464	1	SPN5_SCHPO	P48010	schizosacch
46	5	62.5	465	1	SELA_DESBA	P56372	desulfovibr
47	5	62.5	477	1	DLD2_PSEPU	P31052	pseudomonas
48	5	62.5	534	1	VL1_HPV41	P27557	human papil
49	5	62.5	606	1	GAB_DROME	P25123	drosophila
50	5	62.5	627	1	NDT8_YEAST	P38830	saccharomyc
51	5	62.5	640	1	SEN1_MOUSE	P59110	mus musculu
52	5	62.5	708	1	TRAB_HUMAN	Q9ugi0	homo sapien
53	5	62.5	905	1	CHO2_SCHPO	O74787	schizosacch
54	5	62.5	927	1	CC15_SCHPO	Q09822	schizosacch
55	5	62.5	1795	1	ESP1_HUMAN	Q14674	homo sapien
56	5	62.5	2245	1	MYSJ_DICDI	P54697	dictyosteli
57	5	62.5	2960	1	AHNK_HUMAN	Q09666	homo sapien
58	5	62.5	4451	1	GRSB_BACBR	P14688	b gramicidi
59	4	50.0	52	1	RUBR_MEGEL	P00271	megasphaera
60	4	50.0	61	1	TBA4_MAIZE	P33626	zea mays (m
61	4	50.0	67	1	ATPE_SCHPO	P87316	schizosacch
62	4	50.0	72	1	YA94_ARCFU	O29171	archaeoglob
63	4	50.0	73	1	PHD_BPP1	Q06253	bacterioph
64	4	50.0	75	1	ATPL_RHORU	P15014	rhodospiril
65	4	50.0	75	1	Y14E_BPT4	P39508	bacterioph
66	4	50.0	75	1	Y14E_BPT6	Q38168	bacterioph
67	4	50.0	76	1	TATA_PASMU	Q9ckd3	pasteurella
68	4	50.0	77	1	VG68_BPMD2	O64260	mycobacteri
69	4	50.0	83	1	U222_HUMAN	P60002	homo sapien
70	4	50.0	83	1	U222_MOUSE	P60003	mus musculu
71	4	50.0	86	1	MINE_AGRT5	Q8uax0	agrobacteri
72	4	50.0	87	1	DBI5_BOVIN	Q9mzg3	bos taurus
73	4	50.0	87	1	DBI5_MOUSE	O09035	mus musculu
74	4	50.0	87	1	DBI5_RAT	P56702	rattus norv

75	4	50.0	89	1	TATA_HAEIN	P57046	haemophilus
76	4	50.0	90	1	MINE_BRUME	Q8ybh5	brucella me
77	4	50.0	92	1	KM11_TRYBB	Q26773	trypanosoma
78	4	50.0	92	1	KM11_TRYCR	Q9u6z1	trypanosoma
79	4	50.0	92	1	Y082_METMA	Q8q0q4	methanosarc
80	4	50.0	92	1	YW35_METAC	Q8tl08	methanosarc
81	4	50.0	94	1	CH10_CLOTM	P48223	clostridium
82	4	50.0	94	1	CH10_LACLA	P37283	lactococcus
83	4	50.0	94	1	CH10_LACLC	Q9aep8	lactococcus
84	4	50.0	95	1	PRVA_CAVPO	P51434	cavia porce
85	4	50.0	96	1	CTC2_ACILW	O33951	acinetobact
86	4	50.0	100	1	CBIN_ANASP	Q8yq90	anabaena sp
87	4	50.0	103	1	THIO_LISMO	Q9s386	listeria mo
88	4	50.0	104	1	RS10_AQUAE	O66430	aquifex aeo
89	4	50.0	104	1	RS10_AQUPY	Q9zi51	aquifex pyr
90	4	50.0	107	1	T2AH_DROME	Q9w5b9	drosophila
91	4	50.0	107	1	YAC2_METSO	P27097	methanothri
92	4	50.0	109	1	THI2_SYNY3	P73263	synechocyst
93	4	50.0	110	1	THI2_ANASP	P20857	anabaena sp
94	4	50.0	114	1	Y364_METJA	Q57810	methanococc
95	4	50.0	119	1	YDAY_ECOLI	P76069	escherichia
96	4	50.0	120	1	YACL_SHIFL	P59396	shigella fl
97	4	50.0	123	1	AZUP_PARDE	P80649	paracoccus
98	4	50.0	131	1	CAIF_ECOLI	Q47081	escherichia
99	4	50.0	134	1	FUR_PSEAE	Q03456	pseudomonas
100	4	50.0	134	1	FUR_PSEPU	Q52083	pseudomonas
101	4	50.0	134	1	YF60_ARCFU	O28712	archaeoglob
102	4	50.0	136	1	RL27_CANAL	Q9p843	candida alb
103	4	50.0	138	1	GCSH_PYRAB	Q9v0g1	pyrococcus
104	4	50.0	138	1	GCSH_PYRHO	O59049	pyrococcus
105	4	50.0	140	1	FLGN_SALTY	P37406	salmonella
106	4	50.0	140	1	YF62_ARCFU	O28710	archaeoglob
107	4	50.0	145	1	AZUP_PARPEN	P80401	paracoccus
108	4	50.0	145	1	DUT_CLOTE	Q895r1	clostridium
109	4	50.0	145	1	YAF4_SCHPO	Q09858	schizosacch
110	4	50.0	148	1	REGQ_BPAPS	Q9tlu3	bacterioph
111	4	50.0	149	1	RECX_AMYMD	Q9rev5	amycolatops
112	4	50.0	150	1	VGD_BPAL3	P08765	bacterioph
113	4	50.0	150	1	Y168_SYNP6	P05675	synechococc
114	4	50.0	153	1	HIS3_RHILO	Q98lq5	rhizobium l
115	4	50.0	154	1	FABZ_SHEON	Q8egg4	shewanella
116	4	50.0	156	1	YF60_HAEIN	P44253	haemophilus
117	4	50.0	157	1	RISB_HAEIN	P45149	haemophilus
118	4	50.0	160	1	GPH_PSESS	P42510	pseudomonas
119	4	50.0	161	1	COAD_AQUAE	O66614	aquifex aeo
120	4	50.0	162	1	YPU1_RHOCA	P26157	rhodobacter
121	4	50.0	164	1	YQHA_ECOL6	Q8fdl6	escherichia
122	4	50.0	164	1	YQHA_ECOLI	P52082	escherichia
123	4	50.0	164	1	YQHA_SALTI	Q8z3q8	salmonella
124	4	50.0	164	1	YQHA_SALTY	Q8zml3	salmonella
125	4	50.0	164	1	YT83_RHIME	P29953	rhizobium m
126	4	50.0	165	1	YREP_BUCBP	Q89b48	buchnera ap
127	4	50.0	167	1	DYR_ENTFC	P00380	enterococcu
128	4	50.0	170	1	BMAE_ECOLI	P05818	escherichia
129	4	50.0	172	1	LECA_PLEWA	Q02988	pleurodeles
130	4	50.0	172	1	Y074_NPVOP	O10327	orgyia pseu
131	4	50.0	173	1	TOXS_VIBCH	P24003	vibrio chol

132	4	50.0	173	1	Y150_METJA	Q57614	methanococc
133	4	50.0	174	1	HUPJ_RHILV	P28152	rhizobium l
134	4	50.0	176	1	ARA1_ARAHY	P20780	arachis hyp
135	4	50.0	176	1	FRIM_SALSA	P49947	salmo salar
136	4	50.0	176	1	ISPF_CHLCV	Q824f7	chlamydophi
137	4	50.0	177	1	IF3_ANASP	Q8yne3	anabaena sp
138	4	50.0	177	1	IF3_RHIME	Q92st3	rhizobium m
139	4	50.0	177	1	IF3_SYNY3	P72874	synechocyst
140	4	50.0	177	1	PYRR_FUSNN	Q8rg90	fusobacteri
141	4	50.0	177	1	VP22_ASFB7	P23169	african swi
142	4	50.0	178	1	IF3_BRUME	Q8ye68	brucella me
143	4	50.0	178	1	TRSF_DROER	Q23935	drosophila
144	4	50.0	178	1	YB18_ARCFU	O29147	archaeoglob
145	4	50.0	179	1	YAF4_CAEEL	P52882	caenorhabdi
146	4	50.0	181	1	YG34_MYCPN	P75163	mycoplasma
147	4	50.0	182	1	IF3C_PORPU	P51231	porphyra pu
148	4	50.0	182	1	IF3_SYNEL	Q8dig8	synechococc
149	4	50.0	184	1	TRSF_DROSI	Q24669	drosophila
150	4	50.0	185	1	IF3C_CYACA	Q9tlx8	cyanidium c
151	4	50.0	186	1	EFP_SHEON	Q8eep9	shewanella
152	4	50.0	186	1	RRF_RHOBA	Q7uth0	rhodopirell
153	4	50.0	188	1	KTHY_METJA	Q57741	methanococc
154	4	50.0	189	1	DYR_CAEEL	Q93341	caenorhabdi
155	4	50.0	190	1	GP38_BPSP1	O48394	bacterioph
156	4	50.0	190	1	IF3_PROMP	Q7tu24	prochloroco
157	4	50.0	193	1	RPSH_PSEAE	Q06198	pseudomonas
158	4	50.0	194	1	GRPE_BACHD	Q9kd73	bacillus ha
159	4	50.0	194	1	RS7_FUGRU	P50894	fugu rubrip
160	4	50.0	195	1	Y061_CAUCR	Q9ac08	caulobacter
161	4	50.0	196	1	ELI_PEA	P11432	pisum sativ
162	4	50.0	197	1	OM26_HAEIN	Q57483	haemophilus
163	4	50.0	197	1	TRSF_DROME	P11596	drosophila
164	4	50.0	199	1	IF3_GLOVI	Q7njs6	gloeobacter
165	4	50.0	199	1	PHB1_HUMAN	P31941	homo sapien
166	4	50.0	199	1	UREG_HELPJ	Q9zmz7	helicobacte
167	4	50.0	199	1	UREG_HELPY	Q09066	helicobacte
168	4	50.0	201	1	IF3_PROMA	Q7v9n2	prochloroco
169	4	50.0	202	1	YJ69_ARCFU	O28310	archaeoglob
170	4	50.0	203	1	YBM4_YEAST	P38068	saccharomyc
171	4	50.0	206	1	T2D8_YEAST	Q12030	saccharomyc
172	4	50.0	207	1	KPTA_METAC	Q8th84	methanosarc
173	4	50.0	207	1	KPTA_METMA	Q8pxc3	methanosarc
174	4	50.0	209	1	HOXY_ALCEU	P22319	alcaligenes
175	4	50.0	210	1	RL13 ICTPU	Q90yv5	ictalurus p
176	4	50.0	210	1	TRAW_ECOLI	P18472	escherichia
177	4	50.0	211	1	UREG_ACTPL	O54424	actinobacil
178	4	50.0	217	1	IF3_SYNPX	Q7ua08	synechococc
179	4	50.0	217	1	NFNB_ECOLI	P38489	escherichia
180	4	50.0	217	1	NFNB_SALTY	P15888	salmonella
181	4	50.0	217	1	R10A_SPOFR	Q963b6	spodoptera
182	4	50.0	219	1	IF3_PROMM	Q7tv76	prochloroco
183	4	50.0	222	1	CCG1_HUMAN	Q06432	homo sapien
184	4	50.0	222	1	CCG1_RABIT	P19518	oryctolagus
185	4	50.0	223	1	CCG1_MOUSE	O70578	mus musculu
186	4	50.0	225	1	COX2_RHISA	O99819	hipicephal
187	4	50.0	225	1	MINC_PASMU	P57845	pasteurella
188	4	50.0	225	1	UREG_HAEIN	P44396	haemophilus

189	4	50.0	226	1	GPX3_BOVIN	P37141	bos taurus
190	4	50.0	226	1	GPX3_HUMAN	P22352	homo sapien
191	4	50.0	226	1	GPX3_MOUSE	P46412	mus musculu
192	4	50.0	226	1	GPX3_RAT	P23764	rattus norv
193	4	50.0	227	1	FA3C_HUMAN	Q92520	homo sapien
194	4	50.0	227	1	FA3C_MOUSE	Q91vu0	mus musculu
195	4	50.0	228	1	COX2_ARTSF	Q37706	artemia san
196	4	50.0	228	1	THA2_HUMAN	Q9h0w7	homo sapien
197	4	50.0	229	1	COX2_ALLMI	O47870	alligator m
198	4	50.0	229	1	COX2_ASTPE	Q37411	asterina pe
199	4	50.0	229	1	COX2_PISOC	P25002	pisaster oc
200	4	50.0	229	1	COX2_STRPU	P15545	strongyloce
201	4	50.0	230	1	COX2_BRAFL	O47428	branchiosto
202	4	50.0	230	1	COX2_BRARE	Q9miy7	brachydanio
203	4	50.0	230	1	COX2_GADMO	Q37741	gadus morhu
204	4	50.0	230	1	COX2_POLOR	Q96183	polypterus
205	4	50.0	230	1	T2E7_ECOLI	P50194	escherichia
206	4	50.0	230	1	VNS1_IACKG	P30909	influenza a
207	4	50.0	230	1	VNS1_IADA2	P03501	influenza a
208	4	50.0	230	1	VNS1_IAMA6	P13137	influenza a
209	4	50.0	230	1	VNS1_IAPI1	P13141	influenza a
210	4	50.0	230	1	VNS1_IAPI3	P13143	influenza a
211	4	50.0	230	1	VNS1_IATKB	P30910	influenza a
212	4	50.0	230	1	VNS1_IATKC	P30911	influenza a
213	4	50.0	230	1	VNS1_IATRT	P30912	influenza a
214	4	50.0	231	1	PSD_RICPR	Q9zdt4	rickettsia
215	4	50.0	231	1	PYRH_THEMA	Q9xlu0	thermotoga
216	4	50.0	232	1	Y4IK_RHISN	P55494	rhizobium s
217	4	50.0	233	1	ATE_VIBPA	Q87qy2	vibrio para
218	4	50.0	234	1	NPD_BACTN	Q8a3h9	bacteroides
219	4	50.0	234	1	YAJ8_YEAST	P39548	saccharomyc
220	4	50.0	235	1	RL1_FUSNN	Q8rhi3	fusobacteri
221	4	50.0	238	1	FNR_BACSU	P46908	bacillus su
222	4	50.0	238	1	HS2C_WHEAT	Q00445	triticum ae
223	4	50.0	239	1	COX2_BRALA	O79417	branchiosto
224	4	50.0	239	1	SFSA_AGRT5	P58429	agrobacteri
225	4	50.0	240	1	SRV_SHEEP	Q03257	ovis aries
226	4	50.0	241	1	HFB1_HAEIN	P35757	haemophilus
227	4	50.0	243	1	LEF1_NPVOP	Q65362	orgyia pseu
228	4	50.0	243	1	TONB_ENTAE	P46383	enterobacte
229	4	50.0	243	1	YB35_THETN	Q8rar7	thermoanaer
230	4	50.0	244	1	BID1_PASMU	Q9cn08	pasteurella
231	4	50.0	244	1	MYH7_PAPHA	P11778	papio hamad
232	4	50.0	245	1	YJ54_CLOPE	Q9xdu4	clostridium
233	4	50.0	246	1	YEBC_ECOL6	Q8fgr1	escherichia
234	4	50.0	246	1	YEBC_ECOLI	P24237	escherichia
235	4	50.0	246	1	YEBC_SALTY	Q8xfd4	salmonella
236	4	50.0	246	1	YM15_CLOTE	Q891z5	clostridium
237	4	50.0	247	1	GRAB_HUMAN	P10144	h granzyme
238	4	50.0	247	1	MCT2_MERUN	P50341	meriones un
239	4	50.0	247	1	MCT3_RAT	P50339	rattus norv
240	4	50.0	247	1	MCT5_MOUSE	P21844	mus musculu
241	4	50.0	248	1	YEGW_ECOLI	P76420	escherichia
242	4	50.0	250	1	YFCS_ECOLI	P77599	escherichia
243	4	50.0	251	1	CRB1_HUMAN	P53674	homo sapien
244	4	50.0	251	1	YAT8_SCHPO	Q10153	schizosacch
245	4	50.0	251	1	YQ33_VIBPA	Q87lh9	vibrio para



246	4	50.0	252	1	CRB1_BOVIN	P07318	bos taurus
247	4	50.0	254	1	RECO_BACHD	Q9kd50	bacillus ha
248	4	50.0	259	1	ABCX_CYAPA	P48255	cyanophora
249	4	50.0	259	1	CYAA_BACTY	Q04470	bacillus th
250	4	50.0	259	1	ETFB_CLOAB	P52040	clostridium
251	4	50.0	259	1	PGH1_BOVIN	O62664	bos taurus
252	4	50.0	259	1	PSD_BACHD	Q9kda3	bacillus ha
253	4	50.0	260	1	YG38_METJA	Q59032	methanococc
254	4	50.0	263	1	CYBA_BACTI	Q45723	bacillus th
255	4	50.0	263	1	CYBB_BACTJ	O32322	bacillus th
256	4	50.0	263	1	DIVB_BACSU	P16655	bacillus su
257	4	50.0	265	1	THYX_BORBU	O50965	borrelia bu
258	4	50.0	268	1	YIAJ_HAEIN	P44996	haemophilus
259	4	50.0	269	1	THID_HELPJ	Q9zl00	helicobacte
260	4	50.0	270	1	THID_HELPY	O25515	helicobacte
261	4	50.0	270	1	YA73_METJA	Q58473	methanococc
262	4	50.0	271	1	Y4YP_RHISN	P55724	rhizobium s
263	4	50.0	273	1	Y001_RHIME	Q92tf2	rhizobium m
264	4	50.0	274	1	YKV2_CAEEL	P34324	caenorhabdi
265	4	50.0	275	1	CCG5_MOUSE	Q8vhw4	mus musculu
266	4	50.0	275	1	CCG5_RAT	Q8vhw8	rattus norv
267	4	50.0	275	1	CCG7_HUMAN	Q9bxt1	homo sapien
268	4	50.0	275	1	IF2A_PYRAB	Q9v0e4	pyrococcus
269	4	50.0	275	1	IF2A_PYRFU	Q8ulr5	pyrococcus
270	4	50.0	275	1	IF2A_PYRHO	O58655	pyrococcus
271	4	50.0	276	1	SEGN_HUMAN	O76038	homo sapien
272	4	50.0	276	1	SEGN_MOUSE	Q91wd9	mus musculu
273	4	50.0	279	1	MURI_SYNY3	P73737	synechocyst
274	4	50.0	279	1	RFA2_SCHPO	Q92373	schizosacch
275	4	50.0	279	1	TRPA_BRUME	Q8ye59	brucella me
276	4	50.0	279	1	TRPA_BRUSU	Q8fxy6	brucella su
277	4	50.0	282	1	AQP6_HUMAN	Q13520	homo sapien
278	4	50.0	282	1	MTD_METKA	P94951	methanopyru
279	4	50.0	283	1	GSPK_XANCP	P34026	xanthomonas
280	4	50.0	284	1	SFAS_SPESI	P55925	spermatozop
281	4	50.0	284	1	YRO5_CAEEL	Q09422	caenorhabdi
282	4	50.0	287	1	FRHB_METJA	Q60341	methanococc
283	4	50.0	287	1	KPRS_PYRHO	O59586	pyrococcus
284	4	50.0	288	1	PE12_YEAST	P32854	saccharomyc
285	4	50.0	288	1	YG53_YEAST	P50091	saccharomyc
286	4	50.0	289	1	FMT_MYCPU	Q98rg4	mycoplasma
287	4	50.0	289	1	ISPE_BACAA	Q81vz6	bacillus an
288	4	50.0	289	1	ISPE_BACCR	Q81ja2	bacillus ce
289	4	50.0	289	1	PA1_PROVU	P37447	proteus vul
290	4	50.0	290	1	LEP_HELPY	O25300	helicobacte
291	4	50.0	290	1	YA89_FUSNN	Q8rell	fusobacteri
292	4	50.0	292	1	AMYD_THETU	P37730	thermoanaer
293	4	50.0	292	1	PRMA_PSEPK	Q88dk7	pseudomonas
294	4	50.0	292	1	PRMA_PSESM	Q87vs3	pseudomonas
295	4	50.0	293	1	ADH1_ZEALU	Q07264	zea luxuria
296	4	50.0	293	1	ALF1_PORGI	P60053	porphyromon
297	4	50.0	293	1	BLAC_RHOCA	P14171	rhodobacter
298	4	50.0	293	1	MOTY_VIBAN	Q9s3p9	vibrio angu
299	4	50.0	293	1	RPP1_YEAST	P38786	saccharomyc
300	4	50.0	294	1	FLNB_RABIT	Q9mzd2	oryctolagus
301	4	50.0	294	1	PRMA_PSEAE	Q9huw3	pseudomonas
302	4	50.0	295	1	ALF1_STACA	Q07159	staphylococ

303	4	50.0	295	1	BIEA_RAT	P46844	rattus norv
304	4	50.0	297	1	NADC_HUMAN	Q15274	homo sapien
305	4	50.0	298	1	YIHU_ECOLI	P32142	escherichia
306	4	50.0	299	1	YJ52_STRCO	Q9z513	streptomyce
307	4	50.0	300	1	ALF1_SYNY3	P74309	synechocyst
308	4	50.0	301	1	AFSA_STRGR	P18394	streptomyce
309	4	50.0	301	1	RIPX_MAIZE	P28522	zea mays (m
310	4	50.0	303	1	OPCC_BACSU	O32243	bacillus su
311	4	50.0	304	1	PUR7_PICPA	Q9clj4	pichia past
312	4	50.0	305	1	FMT_UREPA	Q9pq27	ureaplasma
313	4	50.0	305	1	THAB_MOUSE	Q9jjd0	mus musculu
314	4	50.0	306	1	YBFH_BACSU	O31448	bacillus su
315	4	50.0	307	1	P2A5_ARATH	O04951	arabidopsis
316	4	50.0	307	1	PLS2_MOUSE	Q9dcw2	mus musculu
317	4	50.0	311	1	CATA_ACICA	P07773	acinetobact
318	4	50.0	311	1	CC23_TRYBB	P54666	trypanosoma
319	4	50.0	311	1	FMT_MYCGE	P47605	mycoplasma
320	4	50.0	311	1	FMT_MYCPN	P75235	mycoplasma
321	4	50.0	311	1	FMT_STRA3	Q8e754	streptococc
322	4	50.0	312	1	IF2B_DROME	P41375	drosophila
323	4	50.0	312	1	PYRB_COREF	Q8ft39	corynebacte
324	4	50.0	312	1	PYRB_CORGL	Q8nq38	corynebacte
325	4	50.0	313	1	FCN2_HUMAN	Q15485	homo sapien
326	4	50.0	313	1	FMT_ENTFA	Q82zd8	enterococcu
327	4	50.0	313	1	META_VIBCH	Q9krm5	vibrio chol
328	4	50.0	313	1	THAB_HUMAN	Q96ek4	homo sapien
329	4	50.0	314	1	FMT_BUCAP	Q8k974	buchnera ap
330	4	50.0	314	1	HCDH_HUMAN	Q16836	homo sapien
331	4	50.0	316	1	GSHB_XANAC	Q8phz5	xanthomonas
332	4	50.0	316	1	GSHB_XANCP	Q8p6p1	xanthomonas
333	4	50.0	316	1	PRMA_STRR6	Q8dnp4	streptococc
334	4	50.0	317	1	FABD_BACSU	P71019	bacillus su
335	4	50.0	317	1	FMT_LACPL	Q88wl3	lactobacill
336	4	50.0	317	1	MURB_SYNY3	P74529	synechocyst
337	4	50.0	317	1	SOPD_SALTY	P40722	salmonella
338	4	50.0	319	1	ACCL_PETHY	Q08506	petunia hyb
339	4	50.0	319	1	FMT_LACLA	Q9cee9	lactococcus
340	4	50.0	322	1	NADA_AQUAE	O67730	aquifex aeo
341	4	50.0	322	1	SUCA_CAEEL	P53596	caenorhabdi
342	4	50.0	323	1	FRZB_MOUSE	P97401	mus musculu
343	4	50.0	325	1	MOCC_RHIME	P49304	rhizobium m
344	4	50.0	325	1	TRUB_ARCFU	O30001	archaeoglob
345	4	50.0	327	1	PLSX_THEMEA	Q9wxz6	thermotoga
346	4	50.0	329	1	MKK2_CRILO	P49136	cricetulus
347	4	50.0	330	1	RPOS_ECOLI	P13445	escherichia
348	4	50.0	330	1	RPOS_SALTY	P37400	salmonella
349	4	50.0	330	1	RPOS_SHIFL	P35540	shigella fl
350	4	50.0	330	1	VP19_HSVSA	Q01051	herpesvirus
351	4	50.0	331	1	LEU1_THETH	Q56216	thermus the
352	4	50.0	331	1	MURB_ANASP	Q8ym74	anabaena sp
353	4	50.0	331	1	NAHE_PSEPU	Q51947	pseudomonas
354	4	50.0	332	1	DGAL_CITFR	P23925	citrobacter
355	4	50.0	332	1	DGAL_ECOLI	P02927	escherichia
356	4	50.0	332	1	DGAL_SALTY	P23905	salmonella
357	4	50.0	332	1	FLIM_BACSU	P23453	bacillus su
358	4	50.0	332	1	LPXK_HAEIN	P44491	haemophilus
359	4	50.0	332	1	MDHC_BETVU	Q9sml8	beta vulgar

360	4	50.0	332	1	MDHC_MAIZE	Q08062	zea mays (m
361	4	50.0	332	1	MDHC_MESCR	O24047	mesembryant
362	4	50.0	333	1	G3P_HOMAM	P00357	homarus ame
363	4	50.0	333	1	GLPX_HAEIN	P44811	haemophilus
364	4	50.0	333	1	VINT_BPMD2	Q38361	mycobacteri
365	4	50.0	333	1	VINT_BPMFR	P25426	mycobacteri
366	4	50.0	334	1	NAHE_PSEAE	Q57444	pseudomonas
367	4	50.0	334	1	PDXA_BACHD	Q9rc88	bacillus ha
368	4	50.0	334	1	RX1_ASTFA	Q9i9d5	astyanax fa
369	4	50.0	335	1	CITC_HAEIN	P44462	haemophilus
370	4	50.0	335	1	YHBW_ECOLI	P45529	escherichia
371	4	50.0	335	1	YJ53_SCHPO	Q9ut68	schizosacch
372	4	50.0	336	1	PTLS_STRSQ	Q55012	streptomyce
373	4	50.0	336	1	VG27_BPML5	Q05234	mycobacteri
374	4	50.0	337	1	MAT2_COCSA	Q9p445	cochliobolu
375	4	50.0	337	1	MENC_PASMU	Q9clv7	pasteurella
376	4	50.0	339	1	PYRD_HAEIN	P45477	haemophilus
377	4	50.0	339	1	PYRD_PASMU	P57858	pasteurella
378	4	50.0	340	1	RPOA_RICCN	Q92gz0	rickettsia
379	4	50.0	340	1	RPOA_RICPR	Q9zcs9	rickettsia
380	4	50.0	341	1	S122_ARATH	Q9svc2	arabidopsis
381	4	50.0	342	1	YG1L_YEAST	P53219	saccharomyc
382	4	50.0	344	1	CT72_HUMAN	Q9bqp7	homo sapien
383	4	50.0	344	1	PUR5_NEIMA	Q9jua2	neisseria m
384	4	50.0	344	1	PUR5_NEIMB	Q9jz80	neisseria m
385	4	50.0	344	1	RAV1_ARATH	Q9zwm9	arabidopsis
386	4	50.0	344	1	YHJ4_YEAST	P38768	saccharomyc
387	4	50.0	345	1	GPDA_VIBPA	Q87kz2	vibrio para
388	4	50.0	345	1	YL43_SULTO	Q96ym9	sulfolobus
389	4	50.0	346	1	EF1A_EIMBO	Q07051	eimeria bov
390	4	50.0	346	1	PA6A_HUMAN	Q9npb6	homo sapien
391	4	50.0	346	1	PA6A_MOUSE	Q9zl01	mus musculu
392	4	50.0	347	1	GGH_ARATH	O65355	arabidopsis
393	4	50.0	347	1	NTCI_RABIT	Q28727	o ileal sod
394	4	50.0	348	1	AMIE_BACST	Q9rq17	bacillus st
395	4	50.0	348	1	NTCI_RAT	Q62633	r ileal sod
396	4	50.0	350	1	PYRD_FLALU	Q9flu7	flavobacter
397	4	50.0	351	1	HIS8_THETN	Q8r5q4	thermoanaer
398	4	50.0	353	1	CKR8_MOUSE	P56484	mus musculu
399	4	50.0	353	1	PMA1_HUMAN	Q8nd90	homo sapien
400	4	50.0	353	1	PMA1_RAT	Q8vhz4	rattus norv
401	4	50.0	354	1	YCDA_BACSU	O34538	bacillus su
402	4	50.0	357	1	CAD2_ARATH	O49482	arabidopsis
403	4	50.0	357	1	CAD4_TOBAC	P30359	nicotiana t
404	4	50.0	357	1	CAD9_TOBAC	P30360	nicotiana t
405	4	50.0	357	1	CYSA_BACCR	Q81gu1	bacillus ce
406	4	50.0	358	1	CYB_RHISA	O99828	rhhipicephal
407	4	50.0	360	1	CAD1_ARACO	P42495	aralia cord
408	4	50.0	360	1	FLHB_BACSU	P35538	bacillus su
409	4	50.0	360	1	VIS_AGRVI	Q04554	agrobacteri
410	4	50.0	361	1	CADH_LOLPR	O22380	lolium pere
411	4	50.0	361	1	RM45_DROME	Q9vcx3	drosophila
412	4	50.0	361	1	RTC1_DROME	O77264	drosophila
413	4	50.0	361	1	Y101_NPVAC	P25695	autographa
414	4	50.0	363	1	AROB_VIBVU	Q8dcm0	vibrio vuln
415	4	50.0	364	1	ARAR_BACST	Q9s470	bacillus st
416	4	50.0	365	1	RF2_LACLA	Q9cgx1	lactococcus

417	4	50.0	366	1	DP3B_BUCRP	Q9eve4	buchnera ap
418	4	50.0	366	1	YHK0_YEAST	P38772	saccharomyc
419	4	50.0	367	1	VE2_HPV54	Q81021	human papil
420	4	50.0	368	1	AROB_VIBVY	Q7mh84	vibrio vuln
421	4	50.0	368	1	RF2_STRCO	Q53915	streptomyce
422	4	50.0	368	1	YIU5_YEAST	P40577	saccharomyc
423	4	50.0	369	1	DHYS_HUMAN	P49366	homo sapien
424	4	50.0	369	1	YF00_SYNY3	P73003	synechocyst
425	4	50.0	371	1	DHA_MYCTU	P30234	mycobacteri
426	4	50.0	372	1	GPDA_CUPLA	P52425	cuphea lanc
427	4	50.0	374	1	YQK7_CAEEL	Q09289	caenorhabdi
428	4	50.0	375	1	AROB_RHOBA	Q7uwn8	rhodopirell
429	4	50.0	376	1	ADH1_ORYSA	P20306	oryza sativ
430	4	50.0	377	1	TGT_VIBPA	Q87s36	vibrio para
431	4	50.0	378	1	TGT_VIBVU	Q8dey0	vibrio vuln
432	4	50.0	379	1	ADH1_HORVU	P05336	hordeum vul
433	4	50.0	379	1	ADH1_MAIZE	P00333	zea mays (m
434	4	50.0	379	1	ADH1_PENAM	P14219	pennisetum
435	4	50.0	379	1	LPXB_VIBCH	Q9kpw5	vibrio chol
436	4	50.0	379	1	TGT_VIBCH	Q9kty9	vibrio chol
437	4	50.0	380	1	LPXB_VIBVU	Q8dbe8	vibrio vuln
438	4	50.0	380	1	LPXB_VIBVY	Q7mih2	vibrio vuln
439	4	50.0	381	1	KCRB_RABIT	P00567	oryctolagus
440	4	50.0	382	1	FTSZ_BACSU	P17865	bacillus su
441	4	50.0	383	1	FUCO_ECOLI	P11549	escherichia
442	4	50.0	384	1	CARA_RHOGE	Q9jpb87	rhodocyclus
443	4	50.0	384	1	ERD1_KLULA	P41771	kluveromyce
444	4	50.0	384	1	Y297_ANASP	Q8z006	anabaena sp
445	4	50.0	385	1	ALGJ_PSEPK	Q88nd3	pseudomonas
446	4	50.0	385	1	MKK2_MOUSE	P49138	mus musculu
447	4	50.0	385	1	TP6A_AERPE	Q9ye67	aeropyrum p
448	4	50.0	385	1	Y439_PROMP	P59920	prochloroco
449	4	50.0	386	1	CD63_SULTO	Q96yk7	sulfolobus
450	4	50.0	386	1	SUCC_RICCN	Q92i21	rickettsia
451	4	50.0	386	1	SUCC_RICPR	O05966	rickettsia
452	4	50.0	387	1	QIN_AVIS3	P56260	avian sarco
453	4	50.0	387	1	RT05_SCHPO	Q10234	schizosacch
454	4	50.0	388	1	FLHF_BORBU	Q44758	borrelia bu
455	4	50.0	388	1	TRPB_BUCAI	Q44685	buchnera ap
456	4	50.0	389	1	TP6A_SULSH	O05208	sulfolobus
457	4	50.0	393	1	YIP3_YEAST	P40454	saccharomyc
458	4	50.0	395	1	PELO_DROME	P48612	drosophila
459	4	50.0	395	1	PORA_PYRAB	Q9uyz4	pyrococcus
460	4	50.0	395	1	PORA_PYRHO	O73986	pyrococcus
461	4	50.0	396	1	ASSY_HALN1	Q9hmq2	halobacteri
462	4	50.0	396	1	CATE_HUMAN	P14091	homo sapien
463	4	50.0	396	1	DXR_BIFLO	Q8g7y7	bifidobacte
464	4	50.0	396	1	PGK_CAUCR	Q9a3f5	caulobacter
465	4	50.0	396	1	PORA_PYRFU	Q51804	pyrococcus
466	4	50.0	396	1	RF1M_SCHPO	Q09691	schizosacch
467	4	50.0	397	1	DP3B_MYCSM	P52851	mycobacteri
468	4	50.0	397	1	TRPB_NITEU	Q82wi2	nitrosomona
469	4	50.0	397	1	Y435_PROMA	P59918	prochloroco
470	4	50.0	398	1	LPXB_XANCP	Q8paw6	xanthomonas
471	4	50.0	399	1	DP3B_MYCLE	P46387	mycobacteri
472	4	50.0	399	1	DP3B_MYCPA	Q91716	mycobacteri
473	4	50.0	399	1	OYE1_SACPS	Q02899	saccharomyc

474	4	50.0	400	1	MKK2_HUMAN	P49137	homo sapien
475	4	50.0	401	1	PGK_SYNY3	P74421	synechocyst
476	4	50.0	402	1	CN7B_SCHPO	Q09722	schizosacch
477	4	50.0	402	1	DP3B_MYCBO	O33914	mycobacteri
478	4	50.0	402	1	DP3B_MYCTU	Q50790	mycobacteri
479	4	50.0	402	1	RDS1_SCHPO	P53693	schizosacch
480	4	50.0	402	1	SHBG_HUMAN	P04278	homo sapien
481	4	50.0	404	1	NEED_PINRA	O04407	pinus radia
482	4	50.0	405	1	ASSY_THEAC	Q9hkf1	thermoplasm
483	4	50.0	406	1	CG16_HUMAN	Q9y305	homo sapien
484	4	50.0	406	1	IDH_SPHYA	P50215	sphingomona
485	4	50.0	407	1	YEAD_SCHPO	O14078	schizosacch
486	4	50.0	409	1	PGK_METBR	P20972	methanobact
487	4	50.0	410	1	SAHH_THEAC	Q9hxx4	thermoplasm
488	4	50.0	411	1	PROA_WOLSU	Q7m8z4	wolinella s
489	4	50.0	412	1	FABF_ECOLI	P39435	escherichia
490	4	50.0	412	1	PROA_HELHP	Q7vi05	helicobacte
491	4	50.0	413	1	ARJ1_ANASP	Q8yva8	a arginine
492	4	50.0	415	1	KCCS_MALDO	Q07250	malus domes
493	4	50.0	415	1	RHLB_HAEIN	P44922	haemophilus
494	4	50.0	417	1	GLA1_PSEAE	Q9hte9	pseudomonas
495	4	50.0	418	1	GLA2_PSEAE	Q9il38	pseudomonas
496	4	50.0	418	1	LE21_ARCFU	O28316	archaeoglob
497	4	50.0	419	1	DNLI_ASFB7	P35970	african swi
498	4	50.0	419	1	DNLI_ASFM2	P26813	african swi
499	4	50.0	419	1	MUA2_STRPN	Q97qw6	streptococc
500	4	50.0	420	1	PSD4_SCHMA	O17453	schistosoma
501	4	50.0	421	1	DHE2_CLODI	P27346	clostridium
502	4	50.0	421	1	DHE2_PEPAS	P28997	peptostrept
503	4	50.0	422	1	BCHN_ACIRU	Q9wxb4	acidiphiliu
504	4	50.0	422	1	EF1A_METAC	Q8trc4	methanosarc
505	4	50.0	422	1	EF1A_METMA	Q8pur8	methanosarc
506	4	50.0	422	1	TRB1_SULTO	Q971z5	sulfolobus
507	4	50.0	423	1	PHS2_PHALU	Q43617	phaseolus l
508	4	50.0	424	1	DHE2_BACSU	P39633	bacillus su
509	4	50.0	424	1	EF1A_THEAC	P19486	thermoplasm
510	4	50.0	424	1	EF1A_THEVO	Q979t1	thermoplasm
511	4	50.0	424	1	LE22_METJA	P81291	methanococc
512	4	50.0	425	1	ENO_BRUME	Q8yhf0	brucella me
513	4	50.0	425	1	ENO_BRUSU	Q8g0g3	brucella su
514	4	50.0	426	1	CISY_HELPJ	Q9zn37	helicobacte
515	4	50.0	426	1	CISY_HELPY	P56062	helicobacte
516	4	50.0	426	1	G6PI_HALN1	Q9hng6	halobacteri
517	4	50.0	426	1	GSA_ECO57	Q8x4v5	escherichia
518	4	50.0	426	1	GSA_ECOLI	P23893	escherichia
519	4	50.0	426	1	GSA_SALTI	Q8z9b4	salmonella
520	4	50.0	426	1	GSA_SALTY	P21267	salmonella
521	4	50.0	426	1	GSA_YERPE	Q8zbl9	yersinia pe
522	4	50.0	426	1	RAD9_SCHPO	P26306	schizosacch
523	4	50.0	426	1	SYH_LACPL	Q88vq7	lactobacill
524	4	50.0	428	1	GPRX_ORYLA	Q91178	oryzias lat
525	4	50.0	428	1	HEMY_HAEIN	P44772	haemophilus
526	4	50.0	428	1	PHS1_PHALU	P80463	phaseolus l
527	4	50.0	430	1	EF1A_ENTHI	P31018	entamoeba h
528	4	50.0	430	1	SYS_SYNEL	Q8din0	synechococc
529	4	50.0	431	1	HISX_XANCP	Q8p9p2	xanthomonas
530	4	50.0	431	1	SC65_RAT	Q64375	rattus norv

531	4	50.0	432	1	RAD9_SCHOT	P48013	schizosacch
532	4	50.0	433	1	AFLR_EMENI	P52957	emericella
533	4	50.0	434	1	CTPA_BARBA	Q44879	bartonella
534	4	50.0	434	1	GLYA_COREF	Q8fqr1	corynebacte
535	4	50.0	434	1	VG05_VACCC	P21026	vaccinia vi
536	4	50.0	434	1	VG05_VARV	P32995	variola vir
537	4	50.0	437	1	EF1A_AERPE	Q9yav0	aeropyrum p
538	4	50.0	437	1	NO55_HUMAN	Q92791	homo sapien
539	4	50.0	438	1	EF1A_DESMO	P41203	desulfuroco
540	4	50.0	439	1	AC48_MOUSE	Q9r0x4	mus musculu
541	4	50.0	439	1	G6PD_CHLTR	O84188	chlamydia t
542	4	50.0	439	1	IF5Y_ARATH	Q9c8f1	arabidopsis
543	4	50.0	439	1	NH97_CAEEL	Q9bjk5	caenorhabdi
544	4	50.0	439	1	VIT1_DROME	P02843	drosophila
545	4	50.0	439	1	XYLA_CLOTS	P29441	clostridium
546	4	50.0	440	1	ODP2_ZYMMO	O66119	zymomonas m
547	4	50.0	440	1	V117_FOWPV	Q9j5a5	fowlpox vir
548	4	50.0	443	1	FUTB_DROME	Q9v1c1	drosophila
549	4	50.0	444	1	ADRL_DROME	Q9vcy8	drosophila
550	4	50.0	444	1	GLPT_BACSU	P37948	bacillus su
551	4	50.0	444	1	TIG_CAMJE	Q46108	campylobact
552	4	50.0	445	1	NRH3_MOUSE	Q9z0y9	mus musculu
553	4	50.0	445	1	NRH3_RAT	Q62685	rattus norv
554	4	50.0	446	1	HYIN_PSESY	P52831	pseudomonas
555	4	50.0	447	1	EF11_HORVU	P34824	hordeum vul
556	4	50.0	447	1	EF12_DAUCA	P34823	daucus caro
557	4	50.0	447	1	EF12_HORVU	Q40034	hordeum vul
558	4	50.0	447	1	EF1A_MAIZE	Q41803	zea mays (m
559	4	50.0	447	1	EF1A_ORYSA	O64937	oryza sativ
560	4	50.0	447	1	EF1A_PEA	Q41011	pisum sativ
561	4	50.0	447	1	EF1A_SOYBN	P25698	glycine max
562	4	50.0	447	1	EF1A_TOBAC	P43643	nicotiana t
563	4	50.0	447	1	EF1A_VICFA	O24534	vicia faba
564	4	50.0	447	1	EF1A_WHEAT	Q03033	triticum ae
565	4	50.0	447	1	NRH3_HUMAN	Q13133	homo sapien
566	4	50.0	447	1	SYN_LACLA	Q9cek9	lactococcus
567	4	50.0	447	1	SYN_STRPN	Q97pr0	streptococc
568	4	50.0	447	1	SYN_STRR6	Q8cwq4	streptococc
569	4	50.0	447	1	TBB1_DROME	Q24560	drosophila
570	4	50.0	447	1	TBB1_MANSE	O17449	manduca sex
571	4	50.0	448	1	EF1A_LYCES	P17786	lycopersico
572	4	50.0	448	1	HISX_PSESM	Q87wv5	pseudomonas
573	4	50.0	448	1	MURD_PSEAE	Q9hvv9	pseudomonas
574	4	50.0	448	1	SYN_STRA3	Q8e6j1	streptococc
575	4	50.0	448	1	SYN_STRMU	Q8dtm2	streptococc
576	4	50.0	448	1	SYN_STRPY	Q9a0r9	streptococc
577	4	50.0	449	1	EF11_DAUCA	P29521	daucus caro
578	4	50.0	449	1	EF1A_ARATH	P13905	arabidopsis
579	4	50.0	449	1	EF1A_MANES	O49169	manihot esc
580	4	50.0	449	1	MANB_METJA	Q57842	methanococc
581	4	50.0	449	1	TBB_EIMTE	Q27380	eimeria ten
582	4	50.0	450	1	CSK_HUMAN	P41240	homo sapien
583	4	50.0	450	1	CSK_MOUSE	P41241	mus musculu
584	4	50.0	450	1	CSK_RAT	P32577	rattus norv
585	4	50.0	450	1	ENVZ_ECOLI	P02933	escherichia
586	4	50.0	451	1	FXGB_CHICK	Q90964	gallus gall
587	4	50.0	451	1	Y996_METJA	Q58403	methanococc



588	4	50.0	452	1	HOS2_YEAST	P53096	saccharomyc
589	4	50.0	452	1	TIG_CAUCR	O87705	caulobacter
590	4	50.0	453	1	O83A_DROME	Q9vnb3	drosophila
591	4	50.0	454	1	DLDH_RHOCA	P95596	rhodobacter
592	4	50.0	455	1	GUDH_BACSU	P42238	bacillus su
593	4	50.0	455	1	ZPR1_CAEEL	O16999	caenorhabdi
594	4	50.0	456	1	SR54_THEAC	Q9hkt0	thermoplasm
595	4	50.0	457	1	CD4_MOUSE	P06332	mus musculu
596	4	50.0	457	1	VIPR_HUMAN	P32241	homo sapien
597	4	50.0	458	1	GATD_METKA	Q8tv84	methanopyru
598	4	50.0	458	1	VIPR_PIG	Q28992	sus scrofa
599	4	50.0	459	1	NCB1_MOUSE	Q02819	mus musculu
600	4	50.0	459	1	NCB1_RAT	Q63083	rattus norv
601	4	50.0	459	1	ZPR1_SCHPO	O13724	schizosacch
602	4	50.0	460	1	PYRD_ARATH	P32746	arabidopsis
603	4	50.0	461	1	TM15_PIG	Q9tsw0	sus scrofa
604	4	50.0	462	1	LEU2_LISMO	Q8y5r7	listeria mo
605	4	50.0	465	1	FUMC_YERPE	Q8zeb6	yersinia pe
606	4	50.0	465	1	TM15_HUMAN	Q9c019	homo sapien
607	4	50.0	465	1	TM15_PANTR	Q7yr33	pan troglod
608	4	50.0	466	1	FUMC_MYXXA	P95331	myxococcus
609	4	50.0	466	1	SYC_CLOPE	Q8xhq5	clostridium
610	4	50.0	467	1	FUMC_SALTI	Q8z6r6	salmonella
611	4	50.0	468	1	CAC2_YEAST	Q04199	saccharomyc
612	4	50.0	469	1	FXGA_HUMAN	P55316	homo sapien
613	4	50.0	469	1	TRIP_HUMAN	Q9bwf2	homo sapien
614	4	50.0	470	1	PUR1_METJA	Q57657	methanococc
615	4	50.0	470	1	TRIP_MOUSE	Q8vig6	mus musculu
616	4	50.0	471	1	ATPB_HERAU	P42466	herpetosiph
617	4	50.0	471	1	LEU2_VIBPA	Q87ss9	vibrio para
618	4	50.0	471	1	SYC_LISIN	Q92f36	listeria in
619	4	50.0	471	1	SYC_LISMO	Q8yab1	listeria mo
620	4	50.0	472	1	SX14_DROME	P40656	drosophila
621	4	50.0	473	1	FUMC_COREF	Q8fqp8	corynebacte
622	4	50.0	473	1	FUMC_CORGL	Q8nrn8	corynebacte
623	4	50.0	473	1	RGRP_HUMAN	Q8izj4	homo sapien
624	4	50.0	474	1	TRPE_METJA	Q58475	methanococc
625	4	50.0	476	1	3BP5_DROME	Q9v785	drosophila
626	4	50.0	476	1	LEU2_STRCO	O86534	streptomyce
627	4	50.0	477	1	FXGB_HUMAN	P55315	homo sapien
628	4	50.0	477	1	LEU2_STRAW	Q82jr8	streptomyce
629	4	50.0	477	1	SYC_PYRFU	Q8u227	pyrococcus
630	4	50.0	477	1	TIG_BRUME	Q8ygt8	brucella me
631	4	50.0	477	1	TIG_BRUSU	Q8g129	brucella su
632	4	50.0	480	1	EXON_HSV7J	P52346	human herpe
633	4	50.0	480	1	FXGB_RAT	Q00939	rattus norv
634	4	50.0	481	1	FXGB_MOUSE	Q60987	mus musculu
635	4	50.0	481	1	THRC_CORGL	P23669	corynebacte
636	4	50.0	481	1	Y209_ARCFU	O30030	archaeoglob
637	4	50.0	483	1	ARLY_ARCFU	O29379	archaeoglob
638	4	50.0	483	1	ATPB_PRODI	P50003	prochloron
639	4	50.0	483	1	CIMA_METAC	Q8tjj1	methanosarc
640	4	50.0	484	1	SYE_MYCPN	P75114	mycoplasma
641	4	50.0	489	1	ZDS_SYNY3	P74306	synechocyst
642	4	50.0	490	1	YIHF_ECOLI	P32128	escherichia
643	4	50.0	491	1	G6PD_RHIME	Q9z3s2	rhizobium m
644	4	50.0	491	1	GCSB_COXBU	Q83b09	coxiella bu



645	4	50.0	491	1	K2M2_SHEEP	P15241	ovis aries
646	4	50.0	491	1	RNG_HAEIN	P45175	haemophilus
647	4	50.0	491	1	TIG_RHIME	Q92q12	rhizobium m
648	4	50.0	492	1	TIG_AGRT5	Q8ueu0	agrobacteri
649	4	50.0	492	1	TIG_RHILO	Q981e8	rhizobium l
650	4	50.0	492	1	YD48_SCHPO	Q10301	schizosacch
651	4	50.0	494	1	CLS2_STAEP	Q8cnk3	staphylococ
652	4	50.0	494	1	PEA3_BRARE	Q9puq1	brachydanio
653	4	50.0	494	1	PSD3_DROME	P25161	drosophila
654	4	50.0	495	1	ALAT_RAT	P25409	rattus norv
655	4	50.0	495	1	ENGA_YERPE	Q8zct9	yersinia pe
656	4	50.0	496	1	POLG_LIV31	P35764	louping ill
657	4	50.0	496	1	POLG_LIVK	P35765	louping ill
658	4	50.0	496	1	POLG_LIVN1	Q02478	louping ill
659	4	50.0	496	1	POLG_LIVNO	P35766	louping ill
660	4	50.0	496	1	POLG_LIVSB	Q02012	louping ill
661	4	50.0	496	1	PSD3_ANOGA	O61470	anopheles g
662	4	50.0	498	1	VGLY_LYCVA	P09991	lymphocytic
663	4	50.0	499	1	BCHE_SYNY3	Q55373	synechocyst
664	4	50.0	499	1	C771_SOLME	P37123	solanum mel
665	4	50.0	499	1	MURD_RALSO	Q8xvi5	ralstonia s
666	4	50.0	500	1	PSD3_ANOST	Q9u5z8	anopheles s
667	4	50.0	500	1	SYK_BUCBP	Q89ac5	buchnera ap
668	4	50.0	501	1	DLDH_PEA	P31023	pisum sativ
669	4	50.0	502	1	GAG_SIVGB	P22381	simian immu
670	4	50.0	502	1	K2M3_SHEEP	P25691	ovis aries
671	4	50.0	504	1	C6AL_DROME	Q9v774	drosophila
672	4	50.0	504	1	PDA3_MOUSE	P27773	mus musculu
673	4	50.0	505	1	PDA3_BOVIN	P38657	bos taurus
674	4	50.0	505	1	PDA3_HUMAN	P30101	homo sapien
675	4	50.0	505	1	PDA3_RAT	P11598	rattus norv
676	4	50.0	507	1	ATPA_CHLRE	P26526	chlamydomon
677	4	50.0	507	1	CP5G_CANTR	P30609	candida tro
678	4	50.0	507	1	G6PD_CHLMU	Q9pkk8	chlamydia m
679	4	50.0	508	1	2ABA_CANTR	P53031	candida tro
680	4	50.0	511	1	SYK2_METAC	Q8tsn5	methanosarc
681	4	50.0	512	1	G6PD_CHLPN	Q9z8u6	chlamydia p
682	4	50.0	513	1	PDI_HORVU	P80284	hordeum vul
683	4	50.0	513	1	PDI_MAIZE	P52588	zea mays (m
684	4	50.0	518	1	SAP_CHICK	O13035	gallus gall
685	4	50.0	519	1	CPT7_RANDY	O57525	rana dybows
686	4	50.0	520	1	HPAB_KLEOX	Q48440	klebsiella
687	4	50.0	520	1	YM23_MYCTU	Q10508	mycobacteri
688	4	50.0	521	1	REP2_MOUSE	Q80xa6	mus musculu
689	4	50.0	522	1	CEA1_ECOLI	P02978	escherichia
690	4	50.0	522	1	STA_RICCO	Q10710	ricinus com
691	4	50.0	523	1	CP78_SOYBN	O48927	glycine max
692	4	50.0	523	1	TRPE_HALVO	P33975	halobacteri
693	4	50.0	525	1	AGSA_APLCA	P15287	aplysia cal
694	4	50.0	526	1	2ABA_YEAST	Q00362	saccharomyc
695	4	50.0	529	1	VL1_HPV52	Q05138	human papil
696	4	50.0	530	1	AIP2_YEAST	P46681	saccharomyc
697	4	50.0	530	1	PSD3_MOUSE	P14685	mus musculu
698	4	50.0	533	1	LEU1_MICAE	P94907	microcystis
699	4	50.0	533	1	LEU1_SYNY3	P48576	synechocyst
700	4	50.0	533	1	PRI2_DROME	Q9vph2	drosophila
701	4	50.0	534	1	HUP1_CHLKE	P15686	chlorella k

702	4	50.0	534	1	PSD3_HUMAN	O43242	homo sapien
703	4	50.0	534	1	YH39_STRPN	Q97pa2	streptococc
704	4	50.0	535	1	Y475_STRMU	Q8dvk7	streptococc
705	4	50.0	537	1	IR18_MOUSE	Q61098	mus musculu
706	4	50.0	538	1	LEU1_GLOVI	Q7ni93	gloeobacter
707	4	50.0	540	1	SYT_SULTO	Q973c8	sulfolobus
708	4	50.0	543	1	CP1B_MOUSE	Q64429	mus musculu
709	4	50.0	543	1	CP1B_RAT	Q64678	rattus norv
710	4	50.0	543	1	P69_MYCGE	P47533	mycoplasma
711	4	50.0	545	1	LGI2_HUMAN	Q8n0v4	homo sapien
712	4	50.0	546	1	CHK2_MOUSE	Q9z265	mus musculu
713	4	50.0	548	1	CU12_SCHPO	O59755	schizosacch
714	4	50.0	548	1	TRM1_SCHPO	Q9p804	schizosacch
715	4	50.0	550	1	LGI2_MOUSE	Q8k4z0	mus musculu
716	4	50.0	551	1	SYR_MYCGA	Q7nc67	mycoplasma
717	4	50.0	553	1	MCRA_METJA	Q58256	methanococc
718	4	50.0	553	1	SYR_STAAM	Q932f6	staphylococ
719	4	50.0	553	1	SYR_STAAN	Q99w05	staphylococ
720	4	50.0	553	1	SYR_STAAW	Q8nxt8	staphylococ
721	4	50.0	553	1	SYR_STAEP	Q8ctn9	staphylococ
722	4	50.0	554	1	PRP4_ARATH	O22212	arabidopsis
723	4	50.0	555	1	GLPD_BACSU	P18158	bacillus su
724	4	50.0	555	1	MASY_PICAN	P21360	pichia angu
725	4	50.0	555	1	YG62_METJA	Q59056	methanococc
726	4	50.0	557	1	TCPA_DROME	P12613	drosophila
727	4	50.0	558	1	T1MH_METJA	Q60297	methanococc
728	4	50.0	558	1	YNT3_YEAST	P53870	saccharomyc
729	4	50.0	559	1	DNLI_PYRAB	Q9v185	pyrococcus
730	4	50.0	559	1	DNLI_PYRHO	O59288	pyrococcus
731	4	50.0	559	1	DNLI_PYRKO	Q9hhc4	pyrococcus
732	4	50.0	560	1	JI60_HORVU	Q00531	hordeum vul
733	4	50.0	561	1	DNLI_PYRFU	P56709	pyrococcus
734	4	50.0	561	1	IRL2_RAT	Q62929	rattus norv
735	4	50.0	563	1	DEAD_MYCTU	Q11039	mycobacteri
736	4	50.0	563	1	SYR_CLOTE	Q896n5	clostridium
737	4	50.0	563	1	SYR_STRPN	Q54869	streptococc
738	4	50.0	563	1	SYR_STRR6	Q8dn69	streptococc
739	4	50.0	564	1	MASY_SOYBN	P45458	glycine max
740	4	50.0	564	1	SYR_CHLCV	Q824h4	chlamydophi
741	4	50.0	564	1	SYR_LACLA	Q9cel2	lactococcus
742	4	50.0	565	1	DSBD_ECO57	P58162	escherichia
743	4	50.0	565	1	DSBD_ECOLI	P36655	escherichia
744	4	50.0	566	1	XYLR_PSEPU	P06519	pseudomonas
745	4	50.0	567	1	TRA3_MOUSE	Q60803	mus musculu
746	4	50.0	568	1	ERB1_CARAU	Q9w669	carassius a
747	4	50.0	568	1	ESR2_ONCMY	P57782	oncorhynchu
748	4	50.0	571	1	CAN1_CANAL	P43059	candida alb
749	4	50.0	572	1	MOES_LYTVA	P52962	lytechinus
750	4	50.0	575	1	IRL2_HUMAN	Q9hb29	homo sapien
751	4	50.0	576	1	MOES_HUMAN	P26038	homo sapien
752	4	50.0	576	1	MOES_MOUSE	P26041	mus musculu
753	4	50.0	576	1	MOES_PIG	P26042	sus scrofa
754	4	50.0	576	1	MOES_RAT	O35763	rattus norv
755	4	50.0	578	1	MOEH_DROME	P46150	drosophila
756	4	50.0	579	1	Y359_CHLMU	Q9pkv2	chlamydia m
757	4	50.0	580	1	EZRI_BOVIN	P31976	bos taurus
758	4	50.0	583	1	CFAI_HUMAN	P05156	homo sapien

759	4	50.0	583	1	RADI_CHICK	Q9pu45	gallus gall
760	4	50.0	583	1	RADI_HUMAN	P35241	homo sapien
761	4	50.0	583	1	RADI_MOUSE	P26043	mus musculu
762	4	50.0	583	1	RADI_PIG	P26044	sus scrofa
763	4	50.0	583	1	SYR_AQUAE	O67068	aquifex aeo
764	4	50.0	584	1	Y328_CHLPN	Q9z810	chlamydia p
765	4	50.0	585	1	EZRI_HUMAN	P15311	homo sapien
766	4	50.0	585	1	EZRI_MOUSE	P26040	mus musculu
767	4	50.0	585	1	EZRI_RABIT	Q8hza5	oryctolagus
768	4	50.0	585	1	RSD1_LEPIN	P59117	leptospira
769	4	50.0	586	1	KPYK_BACPY	P51182	bacillus ps
770	4	50.0	586	1	MERL_RAT	Q63648	rattus norv
771	4	50.0	587	1	RECN_MYCLE	Q49896	mycobacteri
772	4	50.0	587	1	RECN_MYCTU	O33197	mycobacteri
773	4	50.0	587	1	THIC_CORGL	Q8nqw7	corynebacte
774	4	50.0	591	1	DAK2_SCHPO	O74215	schizosacch
775	4	50.0	591	1	DAK2_YEAST	P43550	saccharomyc
776	4	50.0	591	1	OXAA_HELHP	Q7vjy0	helicobacte
777	4	50.0	593	1	UB22_HUMAN	Q9upt9	homo sapien
778	4	50.0	593	1	VATA_PYRAE	Q8zyr1	pyrobaculum
779	4	50.0	595	1	MERL_HUMAN	P35240	homo sapien
780	4	50.0	595	1	MERL_PAPAN	P59750	papio anubi
781	4	50.0	596	1	APH4_DROME	Q24238	drosophila
782	4	50.0	596	1	MERL_MOUSE	P46662	mus musculu
783	4	50.0	597	1	CHIX_STROI	Q05638	streptomyce
784	4	50.0	598	1	CYL1_HUMAN	P35663	homo sapien
785	4	50.0	598	1	FBL1_CERAE	Q8mjj9	cercopithec
786	4	50.0	598	1	KE04_MOUSE	Q8r151	mus musculu
787	4	50.0	598	1	LEPA_CAMJE	Q9pnrl	campylobact
788	4	50.0	600	1	DNAK_ERYRH	Q05647	erysipeloth
789	4	50.0	600	1	KU70_RHIAP	Q26228	rhhipicephal
790	4	50.0	600	1	LEPA_LEPIN	Q8f500	leptospira
791	4	50.0	600	1	PGH1_SHEEP	P05979	ovis aries
792	4	50.0	602	1	LEPA_OCEIH	Q8cxd0	oceanobacil
793	4	50.0	604	1	DNAK_BACME	P05646	bacillus me
794	4	50.0	606	1	DNAK_BACTR	Q9kws7	bacillus th
795	4	50.0	607	1	DNAK_BACST	Q45551	bacillus st
796	4	50.0	607	1	LEPA_BACAA	Q81lr7	bacillus an
797	4	50.0	607	1	LEPA_BACCR	Q818e4	bacillus ce
798	4	50.0	607	1	LEPA_LACLA	Q9cgi8	lactococcus
799	4	50.0	607	1	LEPA_STAAM	Q99tr4	staphylococ
800	4	50.0	607	1	LEPA_STAAW	Q8nwa7	staphylococ
801	4	50.0	607	1	LEPA_STAEP	Q8cp13	staphylococ
802	4	50.0	607	1	LEPA_STRPN	Q97qk5	streptococc
803	4	50.0	607	1	LEPA_STRR6	Q8dpn5	streptococc
804	4	50.0	608	1	GLMS_SHEON	Q8cx33	s glucosami
805	4	50.0	608	1	LEPA_LISIN	Q92bn4	listeria in
806	4	50.0	608	1	LEPA_LISMO	Q8y742	listeria mo
807	4	50.0	608	1	WDR1_XENLA	Q9w7f2	xenopus lae
808	4	50.0	609	1	FRI_ARATH	Q9fdw0	arabidopsis
809	4	50.0	609	1	LEPA_BACHD	Q9kd76	bacillus ha
810	4	50.0	609	1	WDR1_CHICK	O93277	gallus gall
811	4	50.0	609	1	YKD6_CAEEL	Q03564	caenorhabdi
812	4	50.0	610	1	CHIT_STRPL	P11220	streptomyce
813	4	50.0	610	1	DNAK_STAAM	Q99tr7	staphylococ
814	4	50.0	610	1	DNAK_STAAU	P45554	staphylococ
815	4	50.0	610	1	LEPA_STRA3	Q8e5r3	streptococc

816	4	50.0	610	1	LEPA_STRP3	Q8k7m8	streptococc
817	4	50.0	610	1	LEPA_STRPY	Q99zv8	streptococc
818	4	50.0	611	1	DNAK_BACAA	Q81ls2	bacillus an
819	4	50.0	611	1	DNAK_BACCR	Q818e9	bacillus ce
820	4	50.0	611	1	LEPA_ENTFA	Q831z0	enterococcu
821	4	50.0	611	1	LEPA_STRMU	Q8dtf3	streptococc
822	4	50.0	612	1	DNAK_LISIN	Q92bn8	listeria in
823	4	50.0	612	1	DNAK_LISMO	Q9s5a4	listeria mo
824	4	50.0	612	1	LEPA_BACSU	P37949	bacillus su
825	4	50.0	614	1	PPS2_HUMAN	O95340	h bifunctio
826	4	50.0	616	1	MS2_ARATH	Q08891	arabidopsis
827	4	50.0	617	1	THRB_RAT	P18292	rattus norv
828	4	50.0	618	1	PDA4_CAEEL	P34329	caenorhabdi
829	4	50.0	618	1	THRB_MOUSE	P19221	mus musculu
830	4	50.0	619	1	CHIT_STRLI	P36909	streptomyce
831	4	50.0	619	1	LAC1_NEUCR	P06811	neurospora
832	4	50.0	619	1	LAC2_NEUCR	P10574	neurospora
833	4	50.0	620	1	HSCA_PSESM	Q886z7	pseudomonas
834	4	50.0	622	1	SR68_CANFA	Q00004	canis famil
835	4	50.0	624	1	SCC4_YEAST	P40090	saccharomyc
836	4	50.0	625	1	GPD4_ARATH	Q93zw0	arabidopsis
837	4	50.0	625	1	SR68_MOUSE	Q8bma6	mus musculu
838	4	50.0	627	1	SR68_HUMAN	Q9uhb9	homo sapien
839	4	50.0	630	1	COG6_DROME	Q9v564	drosophila
840	4	50.0	631	1	DHM1_PARDE	P12293	paracoccus
841	4	50.0	631	1	DNAK_CAUCR	P20442	caulobacter
842	4	50.0	631	1	DNAK_PASHA	O52064	pasteurella
843	4	50.0	631	1	DNAK_RHOSP	O05700	rhodopseudo
844	4	50.0	632	1	ARPB_ECOLI	P76205	escherichia
845	4	50.0	632	1	DNAK_ACTAC	P71331	actinobacil
846	4	50.0	633	1	DNAK_BRAJA	P94317	bradyrhizob
847	4	50.0	633	1	DNAK_HAEDU	P48209	haemophilus
848	4	50.0	633	1	DNK2_PROMA	Q7v9g2	prochloroco
849	4	50.0	633	1	DNK2_STRAW	Q826f6	streptomyce
850	4	50.0	633	1	DXS_BACSU	P54523	bacillus su
851	4	50.0	634	1	DNAK_HAEIN	P43736	haemophilus
852	4	50.0	634	1	DNAK_PASMU	P57870	pasteurella
853	4	50.0	634	1	DNK2_PROMM	Q7v3t5	prochloroco
854	4	50.0	634	1	DNK2_SYNP7	P50021	synechococc
855	4	50.0	634	1	KPC3_DROME	P13678	drosophila
856	4	50.0	634	1	SYT_XANAC	Q8pje1	xanthomonas
857	4	50.0	635	1	DNAK_VIBCH	O34241	vibrio chol
858	4	50.0	636	1	CA13_RAT	P13941	rattus norv
859	4	50.0	636	1	DNAK_PHOLL	Q7n8y4	photorhabdu
860	4	50.0	636	1	DNAK_VIBVU	Q8df66	vibrio vuln
861	4	50.0	636	1	DNAK_VIBVY	Q7mn85	vibrio vuln
862	4	50.0	636	1	DNAK_YERPE	Q8zim7	yersinia pe
863	4	50.0	636	1	DNK2_SYNY3	P22358	synechocyst
864	4	50.0	637	1	CLI6_RABIT	Q9n2g5	oryctolagus
865	4	50.0	637	1	DNAK_BUCAI	O32464	buchnera ap
866	4	50.0	637	1	DNAK_ECOLI	P04475	escherichia
867	4	50.0	637	1	DNAK_PSEAE	Q9hv43	pseudomonas
868	4	50.0	637	1	DNAK_SALTI	Q8z9r1	salmonella
869	4	50.0	637	1	DNAK_SALTY	Q56073	salmonella
870	4	50.0	637	1	DNAK_VIBPA	Q87rx3	vibrio para
871	4	50.0	637	1	DNAK_VIBPR	Q917z1	vibrio prot
872	4	50.0	637	1	DNK2_SYNPX	Q7u3c4	synechococc

873	4	50.0	638	1	DNAK_BUCAP	Q8k9y8	buchnera ap
874	4	50.0	638	1	DNAK_BUCBP	P59565	buchnera ap
875	4	50.0	638	1	DNAK_GLOVI	Q7ndh1	gloeobacter
876	4	50.0	638	1	DNAK_PSESG	Q9wwg9	pseudomonas
877	4	50.0	638	1	DNAK_PSESM	Q87wp0	pseudomonas
878	4	50.0	638	1	DNAK_SHIFL	Q83mh5	shigella fl
879	4	50.0	638	1	DNAK_XYLFA	Q9pb05	xylella fas
880	4	50.0	638	1	DNAK_XYLFT	Q87bs8	xylella fas
881	4	50.0	638	1	PDA4_MOUSE	P08003	mus musculu
882	4	50.0	639	1	DNAK_SHEON	Q8eht7	shewanella
883	4	50.0	640	1	DNAK_VIBHA	O87384	vibrio harv
884	4	50.0	640	1	DNK2_SYNEL	Q8di58	synechococc
885	4	50.0	641	1	DNAK_METSS	Q9zfc6	methylovoru
886	4	50.0	641	1	DNAK_PSEPK	Q88du2	pseudomonas
887	4	50.0	641	1	DNAK_XANAC	Q8pmb0	xanthomonas
888	4	50.0	641	1	YPVA_BACSU	P50831	bacillus su
889	4	50.0	642	1	DNAK_CHRVO	Q7nxi3	chromobacte
890	4	50.0	642	1	DNAK_XANCP	Q8pak9	xanthomonas
891	4	50.0	643	1	DNAK_CANBF	Q7vql4	candidatus
892	4	50.0	643	1	PDA4_RAT	P38659	rattus norv
893	4	50.0	644	1	DNAK_LEGPN	O32482	legionella
894	4	50.0	644	1	DNAK_NITEU	O06430	nitrosomona
895	4	50.0	645	1	ACS2_PSEAE	Q9hv66	pseudomonas
896	4	50.0	645	1	DNAK_RHOBA	Q7um31	rhodopirell
897	4	50.0	645	1	DNAK_WIGBR	Q8d2q5	wiggleswort
898	4	50.0	645	1	PDA4_HUMAN	P13667	homo sapien
899	4	50.0	647	1	SKO1_YEAST	Q02100	saccharomyc
900	4	50.0	647	1	YC46_HAEIN	P44135	haemophilus
901	4	50.0	648	1	VP3_BPPH6	P11129	bacterioph
902	4	50.0	649	1	HS70_BLAEM	P48720	blastocladi
903	4	50.0	650	1	DNAK_BURCE	P42373	burkholderi
904	4	50.0	652	1	DNAK_RALSO	Q8xw40	ralstonia s
905	4	50.0	654	1	GSH1_CAEEL	Q20117	caenorhabdi
906	4	50.0	655	1	RFA1_CAEEL	Q19537	caenorhabdi
907	4	50.0	656	1	DNAK_COXBU	O87712	coxiella bu
908	4	50.0	656	1	FEM1_CAEEL	P17221	caenorhabdi
909	4	50.0	656	1	SLY1_DROVI	O18637	drosophila
910	4	50.0	658	1	UVRB_HELPJ	Q9zka0	helicobacte
911	4	50.0	658	1	UVRB_HELPY	P94846	helicobacte
912	4	50.0	660	1	TP6B_METJA	Q58434	methanococc
913	4	50.0	661	1	ACSA_LEPIN	Q8eyg2	leptospira
914	4	50.0	663	1	RGP1_YEAST	P16664	saccharomyc
915	4	50.0	663	1	SEP1_SCHPO	O43058	schizosacch
916	4	50.0	664	1	CNG2_RABIT	Q28718	oryctolagus
917	4	50.0	664	1	NU5M_PHYIN	P50366	phytophthor
918	4	50.0	669	1	SELO_HUMAN	Q9bvl4	homo sapien
919	4	50.0	670	1	ACSA_DROME	Q9vp61	drosophila
920	4	50.0	670	1	CU13_HUMAN	O95447	homo sapien
921	4	50.0	673	1	ESR2_MICUN	P57781	micropogoni
922	4	50.0	673	1	SYGB_LACLA	Q9cgk0	lactococcus
923	4	50.0	675	1	BMX_HUMAN	P51813	homo sapien
924	4	50.0	676	1	VATI_ARCFU	O29106	archaeoglob
925	4	50.0	679	1	DNLJ_HAEIN	P43813	haemophilus
926	4	50.0	683	1	SYM_LACPL	Q88z97	lactobacill
927	4	50.0	684	1	NTP2_MCV1	Q98218	molluscum c
928	4	50.0	684	1	SKIL_HUMAN	P12757	homo sapien
929	4	50.0	684	1	SYGB_PSEAE	Q9i7b8	pseudomonas

930	4	50.0	684	1	SYGB_PSEPK	Q88rr9	pseudomonas
931	4	50.0	684	1	SYGB_PSESM	Q88b35	pseudomonas
932	4	50.0	687	1	SYGB_NEIMA	Q9jw67	neisseria m
933	4	50.0	687	1	SYGB_NEIMB	Q9jxq5	neisseria m
934	4	50.0	688	1	CACM_YEAST	P80235	saccharomyc
935	4	50.0	688	1	EFG_CLOPE	Q8xhs1	clostridium
936	4	50.0	688	1	SYGB_ECOL6	Q8xdn7	escherichia
937	4	50.0	688	1	SYGB_ECOLI	P00961	escherichia
938	4	50.0	688	1	SYGB_HAEIN	P43822	haemophilus
939	4	50.0	688	1	SYGB_SALTI	Q8z2b3	salmonella
940	4	50.0	688	1	SYGB_SALTY	Q8zl96	salmonella
941	4	50.0	688	1	SYGB_VIBCH	Q9kvw8	vibrio chol
942	4	50.0	688	1	SYGB_VIBPA	Q87tp8	vibrio para
943	4	50.0	688	1	THIB_XENLA	Q91641	xenopus lae
944	4	50.0	689	1	SYGB_PASMU	P57905	pasteurella
945	4	50.0	689	1	SYGB_YERPE	Q8z9w7	yersinia pe
946	4	50.0	689	1	YUXG_BACSU	P40747	bacillus su
947	4	50.0	690	1	SYGB_BUCAI	P57235	buchnera ap
948	4	50.0	691	1	DNLJ_MYCTU	O53261	mycobacteri
949	4	50.0	693	1	LYS4_YEAST	P49367	saccharomyc
950	4	50.0	693	1	SYGB_VIBVU	Q8ddj7	vibrio vuln
951	4	50.0	693	1	THPA_HUMAN	P42166	homo sapien
952	4	50.0	694	1	DNLJ_MYCLE	O33102	mycobacteri
953	4	50.0	697	1	SYGB_BUCBP	P59573	buchnera ap
954	4	50.0	699	1	KI22_STRPU	P46872	strongyloce
955	4	50.0	700	1	GPK1_DROME	P32865	drosophila
956	4	50.0	702	1	GLGB_HUMAN	Q04446	homo sapien
957	4	50.0	704	1	CLI6_HUMAN	Q96ny7	homo sapien
958	4	50.0	704	1	ICA_PIG	Q29545	sus scrofa
959	4	50.0	711	1	ORC3_HUMAN	Q9ubd5	homo sapien
960	4	50.0	714	1	YFE7_YEAST	P43556	saccharomyc
961	4	50.0	715	1	GELS_HALRO	O61270	halocynthia
962	4	50.0	715	1	ORC3_MOUSE	Q9jk30	mus musculu
963	4	50.0	719	1	FRE4_YEAST	P53746	saccharomyc
964	4	50.0	723	1	YHJ1_YEAST	P38766	saccharomyc
965	4	50.0	726	1	YB1D_SCHPO	P87178	schizosacch
966	4	50.0	727	1	RBT2_HUMAN	Q9byz6	homo sapien
967	4	50.0	728	1	RBT2_MOUSE	Q91v93	mus musculu
968	4	50.0	730	1	GELS_HORSE	Q28372	equus cabal
969	4	50.0	730	1	ROM_HUMAN	P52272	homo sapien
970	4	50.0	731	1	GLGB_CORGL	Q8nr40	corynebacte
971	4	50.0	735	1	DNLJ_STRCO	Q9z585	streptomyce
972	4	50.0	735	1	FCT_ERWCH	Q47162	erwinia chr
973	4	50.0	739	1	CPSB_ARATH	Q9lkf9	arabidopsis
974	4	50.0	743	1	RELA_HAEIN	P44644	haemophilus
975	4	50.0	744	1	NSF_CRIGR	P18708	cricetulus
976	4	50.0	744	1	NSF_HUMAN	P46459	homo sapien
977	4	50.0	744	1	NSF_MOUSE	P46460	mus musculu
978	4	50.0	745	1	CUL2_HUMAN	Q13617	homo sapien
979	4	50.0	745	1	CUL2_MOUSE	Q9d4h8	mus musculu
980	4	50.0	749	1	NEP_HUMAN	P08473	homo sapien
981	4	50.0	749	1	NEP_MOUSE	Q61391	mus musculu
982	4	50.0	749	1	NEP_RABIT	P08049	oryctolagus
983	4	50.0	749	1	NEP_RAT	P07861	rattus norv
984	4	50.0	749	1	PELX_ERWCH	P22751	erwinia chr
985	4	50.0	749	1	SWAP_CAEEL	Q10580	caenorhabdi
986	4	50.0	755	1	NAPA_DESDE	P81186	desulfovibr



987	4	50.0	757	1	FTSK_LISMO	Q8y7a3	listeria mo
988	4	50.0	760	1	EZ_DROME	P42124	drosophila
989	4	50.0	761	1	FIXI_RHILV	O33533	rhizobium l
990	4	50.0	762	1	FTSK_LISIN	Q92bw9	listeria in
991	4	50.0	762	1	Y961_METJA	Q58371	methanococc
992	4	50.0	767	1	PUB1_SCHPO	Q92462	schizosacch
993	4	50.0	767	1	SYC_YEAST	P53852	saccharomyc
994	4	50.0	769	1	HCRA_THAAR	O33819	thauera aro
995	4	50.0	772	1	GELS_PIG	P20305	sus scrofa
996	4	50.0	775	1	ECEL_HUMAN	O95672	homo sapien
997	4	50.0	775	1	SM3E_HUMAN	O15041	homo sapien
998	4	50.0	775	1	SM3E_MOUSE	P70275	mus musculu
999	4	50.0	775	1	VP4_ROTFL	P39034	feline rota
1000	4	50.0	775	1	VP4_ROTH3	P39033	human rotav

# ALIGNMENTS

## RESULT 1

### A4\_URSMA

ID A4\_URSMA STANDARD; PRT; 57 AA.  
AC Q29149;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Ursus maritimus (Polar bear) (Thalarctos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
OX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis."  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: Functional neuronal receptor which couples to  
CC intracellular signaling pathway through the GTP-binding protein  
CC G(O) (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the APP family.  
CC -----  
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CC -----  
DR EMBL; X56128; CAA39593.1; -.



DR PIR; B60045; B60045.  
 DR HSSP; P05067; 1BA4.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 34 57 POTENTIAL.  
 FT NON\_TER 57 57  
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 8; DB 1; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 0.0091;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

## RESULT 2

### A4\_CANFA

ID A4\_CANFA STANDARD; PRT; 58 AA.  
 AC Q28280;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
 DE protein (Beta-APP) (A-beta)] (Fragment).  
 GN APP.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
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CC -----

DR EMBL; X56125; CAA39590.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 58 POTENTIAL.  
FT NON\_TER 58 58  
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 8; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0092;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 3 EVKMDAEF 10

### RESULT 3

#### A4\_RABIT

ID A4\_RABIT STANDARD; PRT; 58 AA.  
AC Q28748;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis."  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
CC -!- FUNCTION: Functional neuronal receptor which couples to  
CC intracellular signaling pathway through the GTP-binding protein  
CC G(O) (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the APP family.  
CC -----

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CC -----

DR EMBL; X56129; CAA39594.1; -.  
DR HSSP; P05067; 1BA4.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
FT NON\_TER 1 1  
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 34 57 POTENTIAL.  
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
FT NON\_TER 58 58  
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 8; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 0.0092;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
| | | | | | | |  
Db 2 EVKMDAEF 9

#### RESULT 4

##### A4\_SHEEP

ID A4\_SHEEP STANDARD; PRT; 58 AA.  
AC Q28757;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
DE protein (Beta-APP) (A-beta)] (Fragment).  
GN APP.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=92017079; PubMed=1656157;  
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
RT "Conservation of the sequence of the Alzheimer's disease amyloid  
RT peptide in dog, polar bear and five other mammals by cross-species  
RT polymerase chain reaction analysis."  
RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
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 CC -----  
 DR EMBL; X56130; CAA39595.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 34 57 POTENTIAL.  
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 58 58  
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 8; DB 1; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 0.0092;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMDAEF 8  
 |||||  
 Db 2 EVKMDAEF 9

# RESULT 5

## A4\_BOVIN

ID A4\_BOVIN STANDARD; PRT; 59 AA.  
 AC Q28053;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid  
 DE protein (Beta-APP) (A-beta)] (Fragment).  
 GN APP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;

RX MEDLINE=92017079; PubMed=1656157;  
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis."  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).  
 CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -----  
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 CC -----  
 DR EMBL; X56124; CAA39589.1; -.  
 DR EMBL; X56126; CAA39591.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; PARTIAL.  
 DR PROSITE; PS00320; A4\_INTRA; PARTIAL.  
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.  
 FT NON\_TER 1 1  
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).  
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 58 POTENTIAL.  
 FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).  
 FT NON\_TER 59 59  
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 8; DB 1; Length 59;  
 Best Local Similarity 100.0%; Pred. No. 0.0093;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 3 EVKMDAEF 10

#### RESULT 6

##### A4\_SAISC

ID A4\_SAISC STANDARD; PRT; 751 AA.  
 AC Q95241;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid  
 DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble  
 DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);  
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-

DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)  
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-  
 DE secretase C-terminal fragment 50); C31].  
 GN APP.  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney, and Liver;  
 RX MEDLINE=96108492; PubMed=8532114;  
 RA Levy E., Amorim A., Frangione B., Walker L.C.;  
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with  
 RT cerebral amyloid angiopathy."  
 RL Neurobiol. Aging 16:805-808(1995).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP (By  
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction. In vitro, copper-metallated APP induces neuronal  
 CC death directly or is potentiated through Cu(II)-mediated low-  
 CC density lipoprotein oxidation (By similarity). Can regulate  
 CC neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I and IV (By  
 CC similarity). The splice isoforms that contain the BPTI domain  
 CC possess protease inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete  
 CC maturation occurs (O-glycosylated and sulfated). After alpha-  
 CC secretase cleavage, soluble APP is released into the extracellular  
 CC space and the C-terminal is internalized to endosomes and



lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

CC    -!- ALTERNATIVE PRODUCTS:  
CC        Event=Alternative splicing; Named isoforms=2;  
CC        Comment=Additional isoforms seem to exist;  
CC        Name=APP770;  
CC        IsoId=Q95241-1; Sequence=Displayed;  
CC        Name=APP695;  
CC        IsoId=Q95241-2; Sequence=Not described;

CC    -!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

CC    -!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

CC    -!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

CC    -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

CC    -!- PTM: N- and O-glycosylated (By similarity).

CC    -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

CC    -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

CC    -!- SIMILARITY: Belongs to the APP family.

CC    -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC    -----

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; S81024; AAD14347.1; -.  
 DR HSSP; P05067; 1AAP.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Proteoglycan; Amyloid; Alternative splicing.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 751 A4 PROTEIN.  
 FT CHAIN 18 668 SOLUBLE APP-ALPHA (POTENTIAL).  
 FT CHAIN 18 652 SOLUBLE APP-BETA (POTENTIAL).  
 FT CHAIN 653 751 C99 (POTENTIAL).  
 FT CHAIN 653 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).  
 FT CHAIN 653 692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).  
 FT CHAIN 669 751 C83 (POTENTIAL).  
 FT CHAIN 669 694 P3(42) (POTENTIAL).  
 FT CHAIN 669 692 P3(40) (POTENTIAL).  
 FT CHAIN 693 751 GAMMA-CTF(59) (POTENTIAL).  
 FT CHAIN 695 751 GAMMA-CTF(57) (POTENTIAL).  
 FT CHAIN 702 751 GAMMA-CTF(50) (POTENTIAL).  
 FT CHAIN 721 751 C31 (POTENTIAL).  
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 681 704 POTENTIAL.  
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).  
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.  
 FT DOMAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 363 428 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).  
 FT DOMAIN 713 732 INTERACTION WITH G(O)-ALPHA  
 FT (BY SIMILARITY).  
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 274 280 POLY-THR.  
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION  
 FT (BY SIMILARITY).  
 FT ACT\_SITE 301 302 REACTIVE BOND.  
 FT SITE 652 653 CLEAVAGE (BY BETA-SECRETASE)

FT				(BY SIMILARITY).
FT	SITE	653	654	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	668	669	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	685	685	INVOLVED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	687	687	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	692	693	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	694	695	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT				(BY SIMILARITY).
FT	SITE	738	741	ENDOCYTOSIS SIGNAL.
FT	SITE	740	743	NPXY MOTIF.

Query Match 100.0%; Score 8; DB 1; Length 751;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 649 EVKMDAEF 656

# RESULT 7

## A4\_CAVPO

ID A4\_CAVPO STANDARD; PRT; 770 AA.  
 AC Q60495; Q60496;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);  
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid  
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);  
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-  
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].  
 GN APP.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Liver;  
 RX MEDLINE=97236426; PubMed=9116031;  
 RA Beck M., Mueller D., Bigl V.;  
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and  
 RT alternative splicing."  
 RL Biochim. Biophys. Acta 1351:17-21(1997).  
 RN [2]

RP INTERACTION OF BETA-APP40 WITH APOE.  
 RX MEDLINE=98007700; PubMed=9349544;  
 RA Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,  
 RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;  
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on  
 RT cerebral capillary sequestration and blood-brain barrier transport of  
 RT circulating Alzheimer's amyloid beta.";  
 RL J. Neurochem. 69:1995-2004(1997).  
 RN [3]  
 RP PROCESSING.  
 RX MEDLINE=20084499; PubMed=10619481;  
 RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,  
 RA Bigl V.;  
 RT "Guinea-pig primary cell cultures provide a model to study expression  
 RT and amyloidogenic processing of endogenous amyloid precursor  
 RT protein.";  
 RL Neuroscience 95:243-254(2000).  
 RN [4]  
 RP GAMMA-SECRETASE PROCESSING.  
 RX MEDLINE=20576391; PubMed=11035007;  
 RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,  
 RA Ziani-Cherif C., Onstead L., Sambamurti K.;  
 RT "A novel gamma -secretase assay based on detection of the putative  
 RT C-terminal fragment-gamma of amyloid beta protein precursor.";  
 RL J. Biol. Chem. 276:481-487(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP (By  
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction (By similarity). In vitro, copper-metallated APP  
 CC induces neuronal death directly or is potentiated through Cu(II)-  
 CC mediated low-density lipoprotein oxidation (By similarity). Can  
 CC regulate neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I and IV (By  
 CC similarity). The splice isoforms that contain the BPTI domain  
 CC possess protease inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins  
 CC and apolipoproteins E and J in the CSF and to HDL particles in  
 CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.  
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the  
 CC extracellular matrix and may regulate neurite outgrowth in the  
 CC brain (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA

family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity). Soluble Abeta40 binds all three isoforms of APOE, in vitro and in vivo. When lipidated, ApoE3 appears to be the preferred amyloid binding isoform, while the apoE4 isoform-beta-APP40 complex is capable of being transported across the blood-brain barrier.

-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits (By similarity). During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated) (By similarity). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes (By similarity). Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface (By similarity). APP sorts to the basolateral surface in epithelial cells (By similarity).

-!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Comment=Additional isoforms, missing exons 7,8 and 15, seem to exist. The L-isoforms, missing exon 15, are referred to as appicans;  
 Name=APP770;  
 IsoId=Q60495-1; Sequence=Displayed;  
 Name=APP695;  
 IsoId=Q60495-2; Sequence=VSP\_007221, VSP\_007222;

-!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in brain. The longer isoforms containing the BPTI domain are predominantly expressed in peripheral organs such as muscle and liver.

-!- INDUCTION: Increased levels during neuronal differentiation.

-!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

-!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue (By similarity). The NPXY site is also involved in clathrin-mediated endocytosis.

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)

CC and amyloid-beta 42 (Abeta42), major components of amyloid  
 CC plaques, and the corresponding cytotoxic C-terminal fragments  
 CC (CTFs).  
 CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal  
 CC apoptosis (By similarity).  
 CC -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to  
 CC the L-APP isoforms produces the APP proteoglycan core proteins,  
 CC the appicans (By similarity).  
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
 CC serine residues is neuron-specific (By similarity).  
 CC Phosphorylation can affect APP processing, neuronal  
 CC differentiation and interaction with other proteins.  
 CC -!- PTM: Extracellular binding and reduction of copper, results in a  
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation  
 CC of a disulfide bond (By similarity).  
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
 CC zinc, can induce histidine-bridging between beta-amyloid molecules  
 CC resulting in beta-amyloid-metal aggregates.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC -----  
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 CC -----  
 DR EMBL; X97631; CAA66230.1; -.  
 DR EMBL; X99198; CAA67589.1; -.  
 DR HSSP; P05067; 1BA4.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Proteoglycan; Alternative splicing; Amyloid.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.  
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).  
 FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).  
 FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).  
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).  
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).  
 FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).

FT	CHAIN	688	713	P3(42) (BY SIMILARITY).
FT	CHAIN	688	711	P3(40) (BY SIMILARITY).
FT	CHAIN	712	770	GAMMA-CTF(59) (BY SIMILARITY).
FT	CHAIN	714	770	GAMMA-CTF(57) (BY SIMILARITY).

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.058;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 668 EVKMDAEF 675

# RESULT 8

## A4\_HUMAN

ID A4\_HUMAN STANDARD; PRT; 770 AA.  
 AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;  
 AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease  
 DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-  
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42  
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);  
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)  
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-  
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)  
 DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)  
 DE (Amyloid intracellular domain 50) (AID(50)); C31].  
 GN APP OR A4 OR AD1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=87144572; PubMed=2881207;  
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,  
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;  
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a  
 RT cell-surface receptor."  
 RL Nature 325:733-736(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM APP751).  
 RC TISSUE=Brain;  
 RX MEDLINE=88122639; PubMed=2893289;  
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,  
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,  
 RA Cordell B.;  
 RT "A new A4 amyloid mRNA contains a domain homologous to serine  
 RT proteinase inhibitors."  
 RL Nature 331:525-527(1988).  
 RN [3]



RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RX MEDLINE=89128427; PubMed=2783775;  
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,  
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;  
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid  
 RT is encoded by 16 exons.";  
 RL Nucleic Acids Res. 17:517-522(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM APP770).  
 RX MEDLINE=90236318; PubMed=2110105;  
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;  
 RT "Genomic organization of the human amyloid beta-protein precursor  
 RT gene.";  
 RL Gene 87:257-263(1990).  
 RN [5]  
 RP ERRATUM, AND REVISIONS.  
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;  
 RL Gene 102:291-292(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=92268136; PubMed=1587857;  
 RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,  
 RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;  
 RT "Identification and differential expression of a novel alternative  
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in  
 RT leukocytes and brain microglial cells.";  
 RL J. Biol. Chem. 267:10804-10809(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM APP770).  
 RX MEDLINE=97263807; PubMed=9108164;  
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,  
 RA Saito M., Tsukuni S., Sakaki Y.;  
 RT "A novel method for making nested deletions and its application for  
 RT sequencing of a 300 kb region of human APP locus.";  
 RL Nucleic Acids Res. 25:1802-1808(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (ISOFORM APP639).  
 RC TISSUE=Brain;  
 RX MEDLINE=22744650; PubMed=12859342;  
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;  
 RT "Identification of a novel alternative splicing isoform of human  
 RT amyloid precursor protein gene, APP639.";  
 RL Eur. J. Neurosci. 18:102-108(2003).  
 RN [9]  
 RP SEQUENCE FROM N.A. (ISOFORM APP305).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,



RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [10]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89016647; PubMed=3140222;  
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;  
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)  
 RT encodes a 95-kDa polypeptide.";  
 RL Nucleic Acids Res. 16:9351-9351(1988).  
 RN [11]  
 RP ERRATUM, AND REVISIONS.  
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;  
 RL Nucleic Acids Res. 16:11402-11402(1988).  
 RN [12]  
 RP SEQUENCE OF 1-75 FROM N.A.  
 RX MEDLINE=89165870; PubMed=2538123;  
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;  
 RT "Characterization of the 5'-end region and the first two exons of the  
 RT beta-protein precursor gene.";  
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).  
 RN [13]  
 RP SEQUENCE OF 18-50.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=87250462; PubMed=3597385;  
 RA van Nostrand W.E., Cunningham D.D.;  
 RT "Purification of protease nexin II from human fibroblasts.";  
 RL J. Biol. Chem. 262:8508-8514(1987).  
 RN [14]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).  
 RC TISSUE=Brain;  
 RX MEDLINE=89346754; PubMed=2569763;  
 RA de Sauvage F., Octave J.N.;  
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly  
 RT secreted protein.";  
 RL Science 245:651-653(1989).  
 RN [15]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=87231971; PubMed=3035574;  
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;  
 RT "Molecular cloning and characterization of a cDNA encoding the  
 RT cerebrovascular and the neuritic plaque amyloid peptides.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).  
 RN [16]  
 RP SEQUENCE OF 286-366 FROM N.A.  
 RX MEDLINE=88122640; PubMed=2893290;  
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,

RA Gusella J.F., Neve R.L.;  
 RT "Protease inhibitor domain encoded by an amyloid protein precursor  
 RT mRNA associated with Alzheimer's disease.";  
 RL Nature 331:528-530(1988).  
 RN [17]  
 RP SEQUENCE OF 287-367 FROM N.A.  
 RX MEDLINE=88122641; PubMed=2893291;  
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;  
 RT "Novel precursor of Alzheimer's disease amyloid protein shows  
 RT protease inhibitory activity.";  
 RL Nature 331:530-532(1988).  
 RN [18]  
 RP SEQUENCE OF 507-770 FROM N.A.  
 RC TISSUE=Brain cortex;  
 RX MEDLINE=88124954; PubMed=2893379;  
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,  
 RA Marotta C.A.;  
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer  
 RT disease brain: coding and noncoding regions of the fetal precursor  
 RT mRNA are expressed in the cortex.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).  
 RN [19]  
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.  
 RX MEDLINE=96139497; PubMed=8576160;  
 RA Beher D., Hesse L., Masters C.L., Multhaup G.;  
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and  
 RT mapping of the binding sites on APP and collagen type I.";  
 RL J. Biol. Chem. 271:1613-1620(1996).  
 RN [20]  
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717  
 RP AND AD GLY-717.  
 RX MEDLINE=93236601; PubMed=8476439;  
 RA Denman R.B., Rosenzwaig R., Miller D.L.;  
 RT "A system for studying the effect(s) of familial Alzheimer disease  
 RT mutations on the processing of the beta-amyloid peptide precursor.";  
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).  
 RN [21]  
 RP SEQUENCE OF 656-737 FROM N.A.  
 RX MEDLINE=89392030; PubMed=2675837;  
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,  
 RA Little S.P.;  
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows  
 RT similarity to soybean trypsin inhibitor.";  
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).  
 RN [22]

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.058;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 668 EVKMDAEF 675

RESULT 9  
 A4\_MACFA

ID A4\_MACFA STANDARD; PRT; 770 AA.  
 AC P53601; Q95KN7;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);  
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-  
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);  
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)  
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-  
 DE secretase C-terminal fragment 50); C31].  
 GN APP.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=91273117; PubMed=1905108;  
 RA Podlisny M.B., Tolan D.R., Selkoe D.J.;  
 RT "Homology of the amyloid beta protein precursor in monkey and human  
 RT supports a primate model for beta amyloidosis in Alzheimer's  
 RT disease.";  
 RL Am. J. Pathol. 138:1423-1435(1991).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP (By  
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction. In vitro, copper-metallated APP induces neuronal  
 CC death directly or is potentiated through Cu(II)-mediated low-  
 CC density lipoprotein oxidation (By similarity). Can regulate  
 CC neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I and IV (By  
 CC similarity). The splice isoforms that contain the BPTI domain  
 CC possess protease inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2

CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete  
 CC maturation occurs (O-glycosylated and sulfated). After alpha-  
 CC secretase cleavage, soluble APP is released into the extracellular  
 CC space and the C-terminal is internalized to endosomes and  
 CC lysosomes. Some APP accumulates in secretory transport vesicles  
 CC leaving the late Golgi compartment and returns to the cell  
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm  
 CC and nuclei of neurons (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=APP770;  
 CC IsoId=P53601-1; Sequence=Displayed;  
 CC Name=APP695;  
 CC IsoId=P53601-2; Sequence=VSP\_000010, VSP\_000011;  
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for  
 CC sorting of membrane proteins to the basolateral surface of  
 CC epithelial cells (By similarity).  
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The PID domain-containing proteins which bind APP  
 CC require the YENPTY motif for full interaction. These interactions  
 CC are independent of phosphorylation on the terminal tyrosine  
 CC residue. The NPXY site is also involved in clathrin-mediated  
 CC endocytosis (By similarity).  
 CC -!- PTM: Proteolytically processed under normal cellular conditions.  
 CC Cleavage by alpha-secretase or alternatively by beta-secretase  
 CC leads to generation and extracellular release of soluble APP  
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
 CC retention of corresponding membrane-anchored C-terminal fragments,  
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
 CC yields P3 peptides. This is the major secretory pathway and is  
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
 CC gamma-secretase processing of C99 releases the amyloid beta  
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
 CC major components of amyloid plaques, and the cytotoxic C-terminal  
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
 CC similarity).  
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9  
 CC results in the production of the neurotoxic C31 peptide and the  
 CC increased production of beta-amyloid peptides (By similarity).  
 CC -!- PTM: N- and O-glycosylated (By similarity).  
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
 CC serine residues is neuron-specific. Phosphorylation can affect APP  
 CC processing, neuronal differentiation and interaction with other  
 CC proteins (By similarity).  
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and

CC zinc, can induce histidine-bridging between beta-amyloid molecules  
 CC resulting in beta-amyloid-metal aggregates (By similarity).  
 CC Extracellular zinc-binding increases binding of heparin to APP and  
 CC inhibits collagen-binding (By similarity).  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M58727; AAA36829.1; -.  
 DR EMBL; M58726; AAA36828.1; -.  
 DR HSSP; P05067; 1AAP.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Proteoglycan; Alternative splicing; Amyloid.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.  
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).  
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).  
 FT CHAIN 672 770 C99 (POTENTIAL).  
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).  
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).  
 FT CHAIN 688 770 C83 (POTENTIAL).  
 FT CHAIN 688 713 P3(42) (POTENTIAL).  
 FT CHAIN 688 711 P3(40) (POTENTIAL).  
 FT CHAIN 712 770 GAMMA-CTF(59) (POTENTIAL).  
 FT CHAIN 714 770 GAMMA-CTF(57) (POTENTIAL).  
 FT CHAIN 721 770 GAMMA-CTF(50) (POTENTIAL).  
 FT CHAIN 740 770 C31 (POTENTIAL).  
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 700 723 POTENTIAL.  
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).

FT	DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT	DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA
FT				(BY SIMILARITY).
FT	DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	274	280	POLY-THR.
FT	SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION
FT				(BY SIMILARITY).
FT	ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT	SITE	671	672	CLEAVAGE (BY BETA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT	SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE)
FT				(BY SIMILARITY).
FT	SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION
FT				(BY SIMILARITY).
FT	SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS
FT				(BY SIMILARITY).
FT	SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT				(BY SIMILARITY).
FT	SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT				(BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT				(BY SIMILARITY).
FT	SITE	724	734	BASOLATERAL SORTING SIGNAL
FT				(BY SIMILARITY).
FT	SITE	739	740	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.058;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 668 EVKMDAEF 675

# RESULT 10

## A4\_MOUSE

ID A4\_MOUSE STANDARD; PRT; 770 AA.  
 AC P12023; P97487; P97942; Q99K32;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:  
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99  
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein  
 DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase  
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))  
 DE (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)  
 DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)  
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain  
 DE 50) (AID(50)); C31].  
 GN APP.



OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC TISSUE=Brain;  
 RX MEDLINE=88106489; PubMed=3322280;  
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;  
 RT "Complementary DNA for the mouse homolog of the human amyloid beta  
 RT protein precursor.";  
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).  
 RN [2]  
 RP REVISIONS.  
 RA Yamada T.;  
 RL Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=92096458; PubMed=1756177;  
 RA de Strooper B., van Leuven F., van den Berghe H.;  
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse  
 RT is closer related to its human homolog than previously reported.";  
 RL Biochim. Biophys. Acta 1129:141-143(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM APP695).  
 RC STRAIN=SAMP8; TISSUE=Hippocampus;  
 RX MEDLINE=21130647; PubMed=11235921;  
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,  
 RA Alvarez J., Morley J.E.;  
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid  
 RT precursor protein of senescence accelerated mouse (SAMP8).";  
 RL Biochem. Cell Biol. 79:57-67(2001).  
 RN [5]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RX MEDLINE=92209998; PubMed=1555768;  
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,  
 RA Sakai Y.;  
 RT "Positive and negative regulatory elements for the expression of the  
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";  
 RL Gene 112:189-195(1992).  
 RN [6]  
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).  
 RC TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,



RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain, and Kidney;  
 RX MEDLINE=89149813; PubMed=2493250;  
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;  
 RT "Structure and expression of the alternatively-spliced forms of mRNA  
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein  
 RT precursor.";  
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).  
 RN [8]  
 RP SEQUENCE OF 289-364 FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Placenta;  
 RX MEDLINE=89345111; PubMed=2569710;  
 RA Fukuchi K., Martin G.M., Deeb S.S.;  
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein  
 RT precursor of Mus domesticus.";  
 RL Nucleic Acids Res. 17:5396-5396(1989).  
 RN [9]  
 RP SEQUENCE OF 656-737 FROM N.A.  
 RC STRAIN=129/Sv;  
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,  
 RA Loring J.F., Goate A.M.;  
 RT "Introduction of six mutations into the mouse genome using 'Hit and  
 RT Run' gene-targeting: introduction of familial Alzheimer's disease  
 RT mutations into the mouse amyloid precursor protein gene and  
 RT humanization of the A-beta fragment.";  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [10]  
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.  
 RX MEDLINE=93287808; PubMed=8510506;  
 RA Sola C., Mengod G., Ghatti B., Palacios J.M., Triarhou L.C.;  
 RT "Regional distribution of the alternatively spliced isoforms of beta  
 RT APP RNA transcript in the brain of normal, heterozygous and  
 RT homozygous weaver mutant mice as revealed by in situ hybridization  
 RT histochemistry.";  
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).  
 RN [11]  
 RP INTERACTION WITH KNS2.  
 RX MEDLINE=21010507; PubMed=11144355;  
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;  
 RT "Axonal transport of amyloid precursor protein is mediated by direct  
 RT binding to the kinesin light chain subunit of kinesin-I.";  
 RL Neuron 28:449-459(2000).  
 RN [12]  
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;  
 RP THR-743; TYR-757; ASN-759 AND TYR-762.  
 RX MEDLINE=21408156; PubMed=11517249;  
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,  
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,

RA Kyriakis J.M., Nishimoto I.;  
 RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1  
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";  
 RL J. Neurosci. 21:6597-6607(2001).  
 RN [13]  
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.  
 RX MEDLINE=22028091; PubMed=11912189;  
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;  
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins  
 RT with scaffold proteins of the JNK signaling cascade.";  
 RL J. Biol. Chem. 277:20070-20078(2002).  
 RN [14]  
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.  
 RX MEDLINE=22008109; PubMed=12011466;  
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,  
 RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;  
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid  
 RT precursor protein binds Numb and inhibits Notch signaling.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).  
 RN [15]  
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.  
 RX MEDLINE=21437805; PubMed=11553691;  
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;  
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by  
 RT gamma-secretase is rapidly degraded but distributes partially in a  
 RT nuclear fraction of neurones in culture.";  
 RL J. Neurochem. 78:1168-1178(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions. Can promote transcription activation through binding  
 CC to APBB1/Tip60 and inhibit Notch signaling through interaction  
 CC with Numb. Couples to apoptosis-inducing pathways such as those  
 CC mediated by G(0) and JIP. Inhibits G(0) alpha ATPase activity (By  
 CC similarity). Acts as a kinesin I membrane receptor, mediating the  
 CC axonal transport of beta-secretase and presenilin 1. May be  
 CC involved in copper homeostasis/oxidative stress through copper ion  
 CC reduction. Can regulate neurite outgrowth through binding to  
 CC components of the extracellular matrix such as heparin and  
 CC collagen I and IV (By similarity). The splice isoforms that  
 CC contain the BPTI domain possess protease inhibitor activity (By  
 CC similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind  
 CC only weakly transient metals and have little reducing activity due  
 CC to substitutions of transient metal chelating residues. Beta-APP42  
 CC may activate mononuclear phagocytes in the brain and elicit  
 CC inflammatory responses. Promotes both tau aggregation and TPK II-  
 CC mediated phosphorylation (By similarity).  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis.  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits

CC its serine phosphorylation. Also interacts with GPCR-like protein  
 CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via  
 CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the  
 CC MT-binding domains (By similarity). Associates with microtubules  
 CC in the presence of ATP and in a kinesin-dependent manner (By  
 CC similarity). Interacts, through a C-terminal domain, with GNAO1  
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal  
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.058;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 668 EVKMDAEF 675

# RESULT 11

## A4\_PIG

ID A4\_PIG STANDARD; PRT; 770 AA.  
 AC P79307; Q29023; Q9TUI0;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease  
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);  
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-  
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);  
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)  
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-  
 DE secretase C-terminal fragment 50); C31].  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kimura A., Takahashi T.;  
 RT "Amyloid precursor protein 770.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-136 FROM N.A.  
 RC TISSUE=Small intestine;  
 RA Winteroe A.K., Fredholm M.;  
 RT "Evaluation and characterization of a porcine small intestine cDNA  
 RT library.";  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 667-723 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;  
 RT "Conservation of the sequence of the Alzheimer's disease amyloid  
 RT peptide in dog, polar bear and five other mammals by cross-species  
 RT polymerase chain reaction analysis.";  
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-  
 CC inducing pathways such as those mediated by G(0) and JIP (By  
 CC similarity). Inhibits G(0) alpha ATPase activity (By similarity).  
 CC Acts as a kinesin I membrane receptor, mediating the axonal  
 CC transport of beta-secretase and presenilin 1 (By similarity). May  
 CC be involved in copper homeostasis/oxidative stress through copper  
 CC ion reduction (By similarity). In vitro, copper-metallated APP  
 CC induces neuronal death directly or is potentiated through Cu(II)-  
 CC mediated low-density lipoprotein oxidation (By similarity). Can  
 CC regulate neurite outgrowth through binding to components of the  
 CC extracellular matrix such as heparin and collagen I and IV (By  
 CC similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron (By similarity).

CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the  
 CC endoplasmic reticulum) moves to the Golgi complex where complete  
 CC maturation occurs (O-glycosylated and sulfated). After alpha-  
 CC secretase cleavage, soluble APP is released into the extracellular  
 CC space and the C-terminal is internalized to endosomes and  
 CC lysosomes. Some APP accumulates in secretory transport vesicles  
 CC leaving the late Golgi compartment and returns to the cell  
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm  
 CC and nuclei of neurons (By similarity).

CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for  
 CC sorting of membrane proteins to the basolateral surface of  
 CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-  
 CC phosphorylated proteins is required for the specific binding of  
 CC the PID domain. However additional amino acids either N- or C-  
 CC terminal to the NPXY motif are often required for complete  
 CC interaction. The PID domain-containing proteins which bind APP

CC require the YENPTY motif for full interaction. These interactions  
 CC are independent of phosphorylation on the terminal tyrosine  
 CC residue. The NPXY site is also involved in clathrin-mediated  
 CC endocytosis (By similarity).  
 CC -!- PTM: Proteolytically processed under normal cellular conditions.  
 CC Cleavage by alpha-secretase or alternatively by beta-secretase  
 CC leads to generation and extracellular release of soluble APP  
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the  
 CC retention of corresponding membrane-anchored C-terminal fragments,  
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase  
 CC yields P3 peptides. This is the major secretory pathway and is  
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated  
 CC gamma-secretase processing of C99 releases the amyloid beta  
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),  
 CC major components of amyloid plaques, and the cytotoxic C-terminal  
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By  
 CC similarity).  
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis  
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9  
 CC results in the production of the neurotoxic C31 peptide and the  
 CC increased production of beta-amyloid peptides (By similarity).  
 CC -!- PTM: N- and O-glycosylated (By similarity).  
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and  
 CC serine residues is neuron-specific. Phosphorylation can affect APP  
 CC processing, neuronal differentiation and interaction with other  
 CC proteins (By similarity).  
 CC -!- PTM: Extracellular binding and reduction of copper, results in a  
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation  
 CC of a disulfide bond (By similarity).  
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and  
 CC zinc, can induce histidine-bridging between beta-amyloid molecules  
 CC resulting in beta-amyloid-metal aggregates (By similarity).  
 CC Extracellular zinc-binding increases binding of heparin to APP and  
 CC inhibits collagen-binding (By similarity).  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----

DR EMBL; AB032550; BAA84580.1; -.  
 DR EMBL; Z84022; CAB06313.1; -.  
 DR EMBL; X56127; CAA39592.1; -.  
 DR HSSP; P05067; 1AAP.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR002223; Kunitz\_BPTI.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR ProDom; PD000222; Kunitz\_BPTI; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.



DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;  
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;  
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;  
 KW Amyloid.  
 FT SIGNAL 1 17 BY SIMILARITY.  
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.  
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).  
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).  
 FT CHAIN 672 770 C99 (BY SIMILARITY).  
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).  
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).  
 FT CHAIN 688 770 C83 (BY SIMILARITY).  
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).  
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).  
 FT CHAIN 712 770 GAMMA-CTF(59).  
 FT CHAIN 714 770 GAMMA-CTF(57).  
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).  
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).  
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 700 723 POTENTIAL.  
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 135 155 COPPER-BINDING (BY SIMILARITY).  
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).  
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.  
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).  
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).  
 FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY  
 FT SIMILARITY).  
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 274 280 POLY-THR.  
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION  
 FT (BY SIMILARITY).  
 FT ACT\_SITE 301 302 REACTIVE BOND (BY SIMILARITY).  
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE)  
 FT (BY SIMILARITY).  
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).  
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE)  
 FT (BY SIMILARITY).  
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION  
 FT (BY SIMILARITY).  
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS  
 FT (BY SIMILARITY).  
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)  
 FT (BY SIMILARITY).  
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)  
 FT (BY SIMILARITY).  
 FT SITE 720 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
      |||||||  
Db 668 EVKMDAEF 675

RESULT 12

A4\_RAT

ID A4\_RAT STANDARD; PRT; 770 AA.  
AC P08592;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid  
DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble  
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-  
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);  
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal  
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);  
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].  
GN APP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM APP695).  
RC TISSUE=Brain;  
RX MEDLINE=88312583; PubMed=2900758;  
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,  
RA Seeburg P.H.;  
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern  
RT in rat brain suggests a role in cell contact.";  
RL EMBO J. 7:1365-1370(1988).  
RN [2]  
RP SEQUENCE OF 289-364 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=89183625; PubMed=2648331;  
RA Kang J., Mueller-Hill B.;  
RT "The sequence of the two extra exons in rat preA4.";  
RL Nucleic Acids Res. 17:2130-2130(1989).  
RN [3]  
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.  
RX MEDLINE=21443797; PubMed=11483588;  
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;  
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein  
RT family resembling gamma-secretase-like cleavage of Notch.";  
RL J. Biol. Chem. 276:35235-35238(2001).  
RN [4]  
RP ALTERNATIVE SPLICING.  
RX MEDLINE=96187032; PubMed=8624099;  
RA Sandbrink R., Masters C.L., Beyreuther K.;  
RT "APP gene family. Alternative splicing generates functionally related  
RT isoforms.";  
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).  
RN [5]



RP TISSUE SPECIFICITY OF APPICAN.  
RX MEDLINE=95263526; PubMed=7744833;  
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,  
RA Mytilineou C., Margolis R.U., Robakis N.K.;  
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in  
RT brain and is produced by astrocytes but not by neurons in primary  
RT neural cultures.";  
RL J. Biol. Chem. 270:11839-11844(1995).  
RN [6]

RP TISSUE SPECIFICITY OF ISOFORMS.  
RX MEDLINE=97150061; PubMed=8996834;  
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;  
RT "Expression of the APP gene family in brain cells, brain development  
RT and aging.";  
RL Gerontology 43:119-131(1997).  
RN [7]

RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND  
RP TYR-762.  
RX MEDLINE=99127916; PubMed=9930726;  
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,  
RA Suzuki T., Nairn A.C., Greengard P.;  
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the  
RT Alzheimer's amyloid precursor protein.";  
RL J. Neurochem. 72:549-556(1999).  
RN [8]

RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.  
RX MEDLINE=99162676; PubMed=10024358;  
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouilliot C.,  
RA Valenza C., Prochiantz A., Allinquant B.;  
RT "The amyloid precursor protein interacts with Go heterotrimeric  
RT protein within a cell compartment specialized in signal  
RT transduction.";  
RL J. Neurosci. 19:1717-1727(1999).  
RN [9]

RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.  
RX MEDLINE=95256193; PubMed=7737970;  
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;  
RT "The chondroitin sulfate attachment site of appican is formed by  
RT splicing out exon 15 of the amyloid precursor gene.";  
RL J. Biol. Chem. 270:10388-10391(1995).  
RN [10]

RP BETA-AMYLOID METAL-BINDING.  
RX MEDLINE=99316162; PubMed=10386999;  
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,  
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,  
RA Bush A.I.;  
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen  
RT peroxide through metal ion reduction.";  
RL Biochemistry 38:7609-7616(1999).  
RN [11]

RP BETA-AMYLOID ZINC BINDING.  
RX MEDLINE=99343552; PubMed=10413512;  
RA Liu S.T., Howlett G., Barrow C.J.;  
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation  
RT of the A beta peptide of Alzheimer's disease.";  
RL Biochemistry 38:9373-9378(1999).  
RN [12]

RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF  
 RP GLY-704.  
 RX MEDLINE=21956095; PubMed=11959460;  
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;  
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-  
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";  
 RL Biochim. Biophys. Acta 1586:190-198(2001).  
 RN [13]  
 RP PHOSPHORYLATION.  
 RX MEDLINE=97239592; PubMed=9085254;  
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,  
 RA Greengard P., Suzuki T.;  
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is  
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and  
 RT cultured cells.";  
 RL Mol. Med. 3:111-123(1997).  
 RN [14]  
 RP PHOSPHORYLATION ON SER-730.  
 RX MEDLINE=99262094; PubMed=10329382;  
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,  
 RA Greengard P., Nairn A.C., Suzuki T.;  
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid  
 RT precursor protein at Ser655 by a novel protein kinase.";  
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).  
 RN [15]  
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF  
 RP THR-743.  
 RX MEDLINE=99274744; PubMed=10341243;  
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,  
 RA Kirino Y., Greengard P., Suzuki T.;  
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein  
 RT during neuronal differentiation.";  
 RL J. Neurosci. 19:4421-4427(1999).  
 RN [16]  
 RP PHOSPHORYLATION ON THR-743.  
 RX MEDLINE=20396183; PubMed=10936190;  
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,  
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;  
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor  
 RT protein by cyclin-dependent kinase 5.";  
 RL J. Neurochem. 75:1085-1091(2000).  
 RN [17]  
 RP CARBOHYDRATE STRUCTURE OF APPICAN.  
 RX MEDLINE=21463085; PubMed=11479316;  
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,  
 RA Sugahara K., Robakis N.K.;  
 RT "Appican, the proteoglycan form of the amyloid precursor protein,  
 RT contains chondroitin sulfate E in the repeating disaccharide region  
 RT and 4-O-sulfated galactose in the linkage region.";  
 RL J. Biol. Chem. 276:37155-37160(2001).  
 CC -!- FUNCTION: Functions as a cell surface receptor and performs  
 CC physiological functions on the surface of neurons relevant to  
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in  
 CC cell mobility and transcription regulation through protein-protein  
 CC interactions (By similarity). Can promote transcription activation  
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through  
 CC interaction with Numb (By similarity). Couples to apoptosis-

CC inducing pathways such as those mediated by G(0) and JIP. Inhibits  
 CC G(0) alpha ATPase activity. Acts as a kinesin I membrane receptor,  
 CC mediating the axonal transport of beta-secretase and presenilin 1  
 CC (By similarity). May be involved in copper homeostasis/oxidative  
 CC stress through copper ion reduction. Can regulate neurite  
 CC outgrowth through binding to components of the extracellular  
 CC matrix such as heparin and collagen I and IV (By similarity). The  
 CC splice isoforms that contain the BPTI domain possess protease  
 CC inhibitor activity (By similarity).  
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators  
 CC with metal-reducing activity. Bind transient metals such as  
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind  
 CC only weakly transient metals and have little reducing activity due  
 CC to substitutions of transient metal chelating residues. Beta-APP42  
 CC may activate mononuclear phagocytes in the brain and elicit  
 CC inflammatory responses. Promotes both tau aggregation and TPK II-  
 CC mediated phosphorylation (By similarity).  
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the  
 CC extracellular matrix and may regulate neurite outgrowth in the  
 CC brain.  
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved  
 CC peptides, including C31, are potent enhancers of neuronal  
 CC apoptosis (By similarity).  
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several  
 CC cytoplasmic proteins, including APBB family members, the APBA  
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding  
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also  
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2  
 CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.  
 CC In vitro, it binds MAPT via the MT-binding domains (By  
 CC similarity). Associates with microtubules in the presence of ATP  
 CC and in a kinesin-dependent manner (By similarity). Interacts,  
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds  
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid  
 CC associates with HADH2 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface  
 CC protein that rapidly becomes internalized via clathrin-coated  
 CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 100.0%; Score 8; DB 1; Length 770;  
 Best Local Similarity 100.0%; Pred. No. 0.058;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDAEF 8  
 |||||  
 Db 668 EVKMDAEF 675

# RESULT 13

V091\_FOWPV

ID V091\_FOWPV STANDARD; PRT; 656 AA.  
 AC 072896;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein FPV091.  
 GN FPV091 OR FP01L.

OS Fowlpox virus (FPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Avipoxvirus.  
 OX NCBI\_TaxID=10261;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FP-9 / Isolate HP-440;  
 RX MEDLINE=98451804; PubMed=9778782;  
 RA Pollitt E., Skinner M.A., Heaphy S.;  
 RT "Nucleotide sequence of the 4.3 kbp BamHI-N fragment of fowlpox virus  
 RT FP9.";  
 RL Virus Genes 17:5-9(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20193820; PubMed=10729156;  
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;  
 RT "The genome of fowlpox virus.";  
 RL J. Virol. 74:3815-3831(2000).  
 CC -!- SIMILARITY: Belongs to the poxviruses O1 family.  
 CC -----  
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 CC -----  
 DR EMBL; AJ223385; CAA11289.1; -.  
 DR EMBL; AF198100; AAF44435.1; -.  
 DR InterPro; IPR006732; Pox\_O1.  
 DR Pfam; PF04638; Pox\_O1; 1.  
 DR PIRSF; PIRSF015980; VAC\_O1L; 1.  
 SQ SEQUENCE 656 AA; 77177 MW; 274E70D4E26A6456 CRC64;

Query Match 75.0%; Score 6; DB 1; Length 656;  
 Best Local Similarity 100.0%; Pred. No. 8.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMDA 6  
 |||||  
 Db 384 EVKMDA 389

#### RESULT 14

U222\_DROME

ID U222\_DROME STANDARD; PRT; 82 AA.  
 AC Q8MQI6;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Hypothetical UPF0222 protein CG6244.  
 GN CG6244/CG40228 OR BCDNA:RE67573.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=22426071; PubMed=12537574;  
 RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,  
 RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,  
 RA Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,  
 RA Karpen G.H.;  
 RT "Heterochromatic sequences in a *Drosophila* whole-genome shotgun  
 RT assembly.";  
 RL Genome Biol. 3:RESEARCH0085.1-RESEARCH0085.16(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley; TISSUE=Embryo;

RX MEDLINE=22426066; PubMed=12537569;  
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,  
 RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,  
 RA Rubin G.M., Celniker S.E.;  
 RT "A Drosophila full-length cDNA resource.";  
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).  
 CC -!- SIMILARITY: Belongs to the UPF0222 family.  
 CC -----  
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 CC -----  
 DR EMBL; AY129458; AAM76200.1; -.  
 DR FlyBase; FBgn0036531; CG6244.  
 DR InterPro; IPR007808; DUF701.  
 DR Pfam; PF05129; DUF701; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 82 AA; 9565 MW; 52D5464763E8B236 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
 |||||  
 Db 36 EVKMD 40

# RESULT 15

## U222\_MANSE

ID U222\_MANSE STANDARD; PRT; 82 AA.  
 AC Q9U501;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Hypothetical UPF0222 protein.  
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;  
 OC Sphingidae; Sphinginae; Manduca.  
 OX NCBI\_TaxID=7130;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20099029; PubMed=10620045;  
 RA Robertson H.M., Martos R., Sears C., Todres E.Z., Walden K.O.,  
 RA Nardi J.B.;  
 RT "Diversity of odourant binding proteins revealed by an expressed  
 RT sequence tag project on male Manduca sexta moth antennae.";  
 RL Insect Mol. Biol. 8:501-518(1999).  
 CC -!- SIMILARITY: Belongs to the UPF0222 family.  
 CC -----  
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CC -----

DR EMBL; AF117587; AAF16709.1; -.  
DR InterPro; IPR007808; DUF701.  
DR Pfam; PF05129; DUF701; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 82 AA; 9460 MW; AB889CE023AB4E5C CRC64;

Query Match 62.5%; Score 5; DB 1; Length 82;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMD 5  
| | | | |  
Db 36 EVKMD 40

#### RESULT 16

U222\_CAEEL

ID U222\_CAEEL STANDARD; PRT; 84 AA.  
AC Q9XVZ8;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Hypothetical UPF0222 protein Y54G11A.11 in chromosome II.  
GN Y54G11A.11.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Wallis J.M.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.  
CC -!- SIMILARITY: Belongs to the UPF0222 family.  
CC -----

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CC -----

DR EMBL; AL034488; CAA22454.1; -.  
DR PIR; T27174; T27174.  
DR WormPep; Y54G11A.11; CE22483.  
DR InterPro; IPR007808; DUF701.  
DR Pfam; PF05129; DUF701; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 84 AA; 9667 MW; E996ECFC218D227C CRC64;



Query Match 62.5%; Score 5; DB 1; Length 84;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 36 EVKMD 40

RESULT 17

YF24\_MYCPN

ID YF24\_MYCPN STANDARD; PRT; 168 AA.  
AC P75254;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical UPF0134 protein MPN524 (G12\_orf168).  
GN MPN524 OR MP318.  
OS Mycoplasma pneumoniae.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2104;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 29342 / M129;  
RX MEDLINE=97105885; PubMed=8948633;  
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,  
RA Herrmann R.;  
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
RT pneumoniae.";  
RL Nucleic Acids Res. 24:4420-4449(1996).  
CC -!- SIMILARITY: Belongs to the UPF0134 family.  
CC -----  
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CC -----  
DR EMBL; AE000029; AAB95966.1; -.  
DR PIR; S73644; S73644.  
DR InterPro; IPR002862; DUF16.  
DR Pfam; PF01519; DUF16; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 168 AA; 20110 MW; 0878B81DEB019170 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 168;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
|||||  
Db 124 EVKMD 128

RESULT 18

## YF01\_MYCPN

ID YF01\_MYCPN STANDARD; PRT; 196 AA.  
 AC P75286;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical UPF0134 protein MPN501 (P02\_orf196).  
 GN MPN501 OR MP342.  
 OS Mycoplasma pneumoniae.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=2104;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 29342 / M129;  
 RX MEDLINE=97105885; PubMed=8948633;  
 RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,  
 RA Herrmann R.;  
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
 RT pneumoniae.";  
 RL Nucleic Acids Res. 24:4420-4449(1996).  
 CC -!- SIMILARITY: Belongs to the UPF0134 family.  
 CC -----  
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 CC -----  
 DR EMBL; AE000032; AAB95989.1; -.  
 DR PIR; S73668; S73668.  
 DR InterPro; IPR002862; DUF16.  
 DR Pfam; PF01519; DUF16; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 196 AA; 23165 MW; 165C0E960D1EFF48 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKMD 5  
 |||||  
 Db 166 EVKMD 170

## RESULT 19

## BIOS\_RHIME

ID BIOS\_RHIME STANDARD; PRT; 217 AA.  
 AC 008250;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Biotin transport regulator.  
 GN BIOS OR R01535 OR SMC02061.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=97449848; PubMed=9304864;  
 RA Streit W.R., Phillips D.A.;  
 RT "A biotin-regulated locus, bioS, in a possible survival operon of  
 RT Rhizobium meliloti.";  
 RL Mol. Plant Microbe Interact. 10:933-937(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,  
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=99424419; PubMed=10494632;  
 RA Heinz E.B., Phillips D.A., Streit W.R.;  
 RT "BioS, a biotin-induced, stationary-phase, and possible LysR-type  
 RT regulator in Sinorhizobium meliloti.";  
 RL Mol. Plant Microbe Interact. 12:803-812(1999).  
 CC -!- FUNCTION: MAY BE PART OF A SYSTEM THAT R.MELILOTI USES TO RESPOND  
 CC TO PLANT (ALFALFA) BIOTIN SIGNALS.  
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts  
 CC in positions 123, 135, and 152.  
 CC -!- CAUTION: When this protein is expressed in E.coli it migrates as a  
 CC 36 kDa protein; thus the sequence may be incorrect in the C-  
 CC terminal section.  
 CC -----  
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 CC -----  
 DR EMBL; U81296; AAB88076.1; ALT\_FRAME.  
 DR EMBL; AL591787; CAC46114.1; -.  
 KW Transcription regulation; Complete proteome.  
 SQ SEQUENCE 217 AA; 23827 MW; AEA5E029C076DD80 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8  
 |||||  
 Db 153 MDAEF 157

RESULT 20

HRF1\_NPVLD

ID HRF1\_NPVLD STANDARD; PRT; 218 AA.  
 AC Q90165;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Host range factor 1.  
 GN HRF-1.  
 OS Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=10449;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Hamden;  
 RX MEDLINE=98139158; PubMed=9499118;  
 RA Chen C.J., Quentin M.E., Brennan L.A., Kukel C., Thiem S.M.;  
 RT "Lymantria dispar nucleopolyhedrovirus hrf-1 expands the larval host  
 RT range of Autographa californica nucleopolyhedrovirus."  
 RL J. Virol. 72:2526-2531(1998).  
 CC -!- FUNCTION: Facilitates AcMNPV replication in two non-permissive  
 CC cell lines, IPLB-Ld652Y and IPLB-LdFB.  
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 CC -----  
 DR EMBL; U38895; AAB07701.1; -.  
 DR PIR; T30415; T30415.  
 SQ SEQUENCE 218 AA; 25675 MW; 5DD2BB0E16802001 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 218;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MDAEF 8  
 |||||  
 Db 3 MDAEF 7

RESULT 21

COX2\_ALBCO

ID COX2\_ALBCO STANDARD; PRT; 224 AA.  
 AC P48889;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN COII.  
 OS Albinaria coerulea (Land snail).

OG Mitochondrion.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Clausilioidea; Clausiliidae; Alopinae; Albinaria.  
 OX NCBI\_TaxID=42349;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96120351; PubMed=7498775;  
 RA Hatzoglou E., Rodakis G.C., Lecanidou R.;  
 RT "Complete sequence and gene organization of the mitochondrial genome  
 RT of the land snail Albinaria coerulea.";  
 RL Genetics 140:1353-1366(1995).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
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 CC -----  
 DR EMBL; X83390; CAA58300.1; -.  
 DR PIR; S59147; S59147.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 PROBABLE.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 PROBABLE.  
 FT DOMAIN 83 224 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 224 AA; 25246 MW; BD1BC99250F2429A CRC64;

Query Match 62.5%; Score 5; DB 1; Length 224;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

RESULT 22

COX2\_ALBTU

ID COX2\_ALBTU STANDARD; PRT; 224 AA.  
AC Q09334;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
GN COII.  
OS Albinaria turrita (Door snail).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Clausilioidea; Clausiliidae; Alopinae; Albinaria.  
OX NCBI\_TaxID=27820;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94275881; PubMed=8007005;  
RA Lecanidou R., Douris V., Rodakis G.C.;  
RT "Novel features of metazoan mtDNA revealed from sequence analysis of  
RT three mitochondrial DNA segments of the land snail Albinaria turrita  
RT (Gastropoda: Clausiliidae).";  
RL J. Mol. Evol. 38:369-382(1994).  
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- COFACTOR: Copper A.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane.  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
CC -----  
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CC -----  
DR EMBL; X71395; CAA50517.1; -.  
DR InterPro; IPR001505; Copper\_CuA.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
DR Pfam; PF00116; COX2; 1.  
DR Pfam; PF02790; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXIDASEII.  
DR ProDom; PD000131; Copper\_CuA; 1.  
DR PROSITE; PS00078; COX2; 1.

KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
KW Electron transport; Respiratory chain.  
FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
FT TRANSMEM 27 48 PROBABLE.  
FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
FT TRANSMEM 63 82 PROBABLE.  
FT DOMAIN 83 224 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
FT METAL 161 161 COPPER A (PROBABLE).  
FT METAL 196 196 COPPER A (PROBABLE).  
FT METAL 200 200 COPPER A (PROBABLE).  
FT METAL 204 204 COPPER A (PROBABLE).  
SQ SEQUENCE 224 AA; 25091 MW; 5D44CC670932075A CRC64;

Query Match 62.5%; Score 5; DB 1; Length 224;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

# RESULT 23

## COX2\_PARLI

ID COX2\_PARLI STANDARD; PRT; 229 AA.  
AC P12701;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
GN COII.  
OS Paracentrotus lividus (Common sea urchin).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;  
OC Paracentrotus.  
OX NCBI\_TaxID=7656;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Egg;  
RX MEDLINE=89291831; PubMed=2544576;  
RA Cantatore P., Roberti M., Rainaldi G., Gadaleta M.N., Saccone C.;  
RT "The complete nucleotide sequence, gene organization, and genetic  
RT code of the mitochondrial genome of Paracentrotus lividus.";  
RL J. Biol. Chem. 264:10965-10975(1989).  
RN [2]  
RP SEQUENCE OF 1-11 FROM N.A.  
RC TISSUE=Egg;  
RX MEDLINE=87248108; PubMed=3596250;  
RA Cantatore P., Roberti M., Morisco P., Rainaldi G., Gadaleta M.N.,  
RA Saccone C.;  
RT "A novel gene order in the Paracentrotus lividus mitochondrial  
RT genome.";  
RL Gene 53:41-54(1987).  
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2



CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; J04815; AAA68137.1; -.  
 DR EMBL; M16520; AAA31991.1; -.  
 DR PIR; E34284; E34284.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 POTENTIAL.  
 FT DOMAIN 83 229 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 FT CONFLICT 9 9 L -> P (IN REF. 2).  
 FT CONFLICT 11 11 D -> H (IN REF. 2).  
 SQ SEQUENCE 229 AA; 26045 MW; 9FEC52A0EDDB48A0 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

RESULT 24  
 COX2\_CARAU  
 ID COX2\_CARAU STANDARD; PRT; 230 AA.  
 AC 078682;  
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN COXII OR COII.  
 OS Carassius auratus (Goldfish).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_TaxID=7957;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AZ3 / Langsdorfi; TISSUE=Oocyte;  
 RA Murakami M., Yamashita Y., Fujitani H.;  
 RT "The complete sequence of mitochondrial genome from a gynogenetic  
 RT triploid 'ginbuna' (Carassius auratus langsdorfi).";  
 RL Zool. Sci. 15:335-337(1998).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; AB006953; BAA31241.1; -.  
 DR HSSP; P18400; 1CYX.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 PROBABLE.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 PROBABLE.  
 FT DOMAIN 83 230 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).

FT METAL 204 204 COPPER A (PROBABLE).  
SQ SEQUENCE 230 AA; 26045 MW; 39A0B54FE31B2377 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 230;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

RESULT 25

COX2\_CROLA

ID COX2\_CROLA STANDARD; PRT; 230 AA.  
AC P34189;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
GN COXII OR COII.  
OS Crossostoma lacustre (Oriental stream loach).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Balitoridae; Crossostoma.  
OX NCBI\_TaxID=7980;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93027205; PubMed=1408800;  
RA Tzeng C.-S., Hui C.-F., Shen S.-C., Huang P.C.;  
RT "The complete nucleotide sequence of the Crossostoma lacustre  
RT mitochondrial genome: conservation and variations among  
RT vertebrates."  
RL Nucleic Acids Res. 20:4853-4858(1992).  
CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
CC 3 form the functional core of the enzyme complex. Subunit 2  
CC transfers the electrons from cytochrome c via its binuclear copper  
CC A center to the bimetallic center of the catalytic subunit 1.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- COFACTOR: Copper A.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane.  
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
CC -----  
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CC -----  
DR EMBL; M91245; AAB96814.1; -.  
DR PIR; S35465; S35465.

DR HSSP; P18400; 1CYX.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 POTENTIAL.  
 FT DOMAIN 83 230 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 230 AA; 26093 MW; 73D11DE016194329 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 26

## COX2\_CYPCA

ID COX2\_CYPCA STANDARD; PRT; 230 AA.  
 AC P24987;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN MTCO2 OR COXII OR COII.  
 OS Cyprinus carpio (Common carp).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94223691; PubMed=8169959;  
 RA Chang Y.S., Huang F.L., Lo T.B.;  
 RT "The complete nucleotide sequence and gene organization of carp  
 (Cyprinus carpio) mitochondrial genome."  
 RL J. Mol. Evol. 38:138-155(1994).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper

CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; X61010; CAA43340.1; -.  
 DR PIR; S36009; S36009.  
 DR HSSP; P18400; 1CYX.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 POTENTIAL.  
 FT DOMAIN 83 230 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 230 AA; 25999 MW; 237E10E13DBDDFED CRC64;

Query Match 62.5%; Score 5; DB 1; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

RESULT 27  
 COX2\_ONCMY  
 ID COX2\_ONCMY STANDARD; PRT; 230 AA.  
 AC P48171;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).

GN COXII OR COII.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96139027; PubMed=8587139;  
 RA Zardoya R., Garrido-Pertierra A., Bautista J.M.;  
 RT "The complete nucleotide sequence of the mitochondrial DNA genome of  
 RT the rainbow trout, Oncorhynchus mykiss."  
 RL J. Mol. Evol. 41:942-951(1995).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; L29771; AAB03350.1; -.  
 DR PIR; T09860; T09860.  
 DR HSSP; P18400; 1CYX.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 PROBABLE.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 PROBABLE.  
 FT DOMAIN 83 230 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).

SQ SEQUENCE 230 AA; 26029 MW; 51D42ED68BEF16B5 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 230;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
|||||  
Db 170 VKMDA 174

#### RESULT 28

##### COX2\_SALSA

ID COX2\_SALSA STANDARD; PRT; 230 AA.

AC Q37677; Q9MPG8;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).

GN COXII OR COII.

OS Salmo salar (Atlantic salmon).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

OX NCBI\_TaxID=8030;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=20018174; PubMed=10548724;

RA Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;

RT "The complete mitochondrial DNA sequence of the Atlantic salmon, *Salmo salar*.";

RL Gene 239:237-242(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Arnason U., Johnsson E., Rasmussen A.S.;

RT "The complete mitochondrial genome sequence of a teleost, *Salmo salar*, and comparisons with other salmoniformes.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE OF 85-230 FROM N.A.

RC TISSUE=Kidney;

RA Hardiman G.T., Wolff J., Peden J., Gannon F.;

RT "Isolation of Atlantic Salmon (*Salmo salar*) cytochrome c oxidase subunit II gene (coxII).";

RL J. Appl. Ichthyol. 10:64-68(1994).

RN [4]

RP REVISIONS.

RA Hardiman G.T.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory chain that catalyzes the reduction of oxygen to water. Subunits 1-

CC 3 form the functional core of the enzyme complex. Subunit 2

CC transfers the electrons from cytochrome c via its binuclear copper

CC A center to the bimetallic center of the catalytic subunit 1.

CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome



```

CC      c + 2 H(2)O.
CC      -!- COFACTOR: Copper A.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane.
CC      -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U12143; AAD04736.1; -.
DR      EMBL; AF133701; AAF61381.1; -.
DR      EMBL; L04501; AAB08524.1; -.
DR      PIR; T09950; T09950.
DR      HSSP; P18400; 1CYX.
DR      InterPro; IPR001505; Copper_CuA.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR002429; Cyt_c_ox_2.
DR      Pfam; PF00116; COX2; 1.
DR      Pfam; PF02790; COX2_TM; 1.
DR      PRINTS; PR01166; CYCOXIDASEII.
DR      ProDom; PD000131; Copper_CuA; 1.
DR      PROSITE; PS00078; COX2; 1.
KW      Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
KW      Electron transport; Respiratory chain.
FT      DOMAIN      1      26      MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
FT      TRANSMEM      27      48      PROBABLE.
FT      DOMAIN      49      62      MITOCHONDRIAL MATRIX (POTENTIAL).
FT      TRANSMEM      63      82      PROBABLE.
FT      DOMAIN      83     230      MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
FT      METAL       161     161      COPPER A (PROBABLE).
FT      METAL       196     196      COPPER A (PROBABLE).
FT      METAL       200     200      COPPER A (PROBABLE).
FT      METAL       204     204      COPPER A (PROBABLE).
FT      CONFLICT    175     175      S -> V (IN REF. 1).
FT      CONFLICT    209     209      I -> V (IN REF. 3).
FT      CONFLICT    227     230      LEDA -> TW (IN REF. 3).
SQ      SEQUENCE    230 AA;  26016 MW;  405C95AA58112AF4 CRC64;

```

```

Query Match      62.5%;  Score 5;  DB 1;  Length 230;
Best Local Similarity 100.0%;  Pred. No. 54;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 VKMDA 6
        |||||
Db      170 VKMDA 174

```

```

RESULT 29
COX2_SCYCA
ID      COX2_SCYCA      STANDARD;      PRT;      230 AA.
AC      079404;
DT      15-DEC-1998 (Rel. 37, Created)

```

DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN COXII OR COII.  
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX MEDLINE=98393590; PubMed=9725850;  
 RA Delarbre C., Spruyt N., Delmarre C., Gallut C., Barriol V.,  
 RA Janvier P., Laudet V., Gachelin G.;  
 RT "The complete nucleotide sequence of the mitochondrial DNA of the  
 RT dogfish, Scyliorhinus canicula.";  
 RL Genetics 150:331-344(1998).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; Y16067; CAA76022.1; -.  
 DR PIR; T11303; T11303.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 PROBABLE.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 PROBABLE.  
 FT DOMAIN 83 230 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).

FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 230 AA; 26198 MW; 89311D5BD5BF7397 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 30

## COX2\_SQUAC

ID COX2\_SQUAC STANDARD; PRT; 230 AA.  
 AC Q9ZZ51;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN COXII OR COII.  
 OS Squalus acanthias (Spiny dogfish).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.  
 OX NCBI\_TaxID=7797;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99091711; PubMed=9873084;  
 RA Rasmussen A.S., Arnason U.;  
 RT "Phylogenetic studies of complete mitochondrial DNA molecules place  
 RT cartilaginous fishes within the tree of bony fishes."  
 RL J. Mol. Evol. 48:118-123(1999).  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; Y18134; CAA77052.1; -.  
 DR PIR; T11537; T11537.

DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 POTENTIAL.  
 FT DOMAIN 83 230 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 230 AA; 26246 MW; AC04C362577055A4 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 31

## COX2\_LATCH

ID COX2\_LATCH STANDARD; PRT; 231 AA.  
 AC 003848;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN COII.  
 OS Latimeria chalumnae (Latimeria) (Coelacanth).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Coelacanthiformes; Coelacanthidae; Latimeria.  
 OX NCBI\_TaxID=7897;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zardoya R., Meyer A.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial

CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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 CC -----  
 DR EMBL; U82228; AAC60321.1; -.  
 DR InterPro; IPR001505; Copper\_CuA.  
 DR InterPro; IPR008972; Cupredoxin.  
 DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
 DR Pfam; PF00116; COX2; 1.  
 DR Pfam; PF02790; COX2\_TM; 1.  
 DR PRINTS; PR01166; CYCOXIDASEII.  
 DR ProDom; PD000131; Copper\_CuA; 1.  
 DR PROSITE; PS00078; COX2; 1.  
 KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
 KW Electron transport; Respiratory chain.  
 FT DOMAIN 1 26 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT TRANSMEM 27 48 POTENTIAL.  
 FT DOMAIN 49 62 MITOCHONDRIAL MATRIX (POTENTIAL).  
 FT TRANSMEM 63 82 POTENTIAL.  
 FT DOMAIN 83 231 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
 FT METAL 161 161 COPPER A (PROBABLE).  
 FT METAL 196 196 COPPER A (PROBABLE).  
 FT METAL 200 200 COPPER A (PROBABLE).  
 FT METAL 204 204 COPPER A (PROBABLE).  
 SQ SEQUENCE 231 AA; 26398 MW; 70FEE6EC09C47FA7 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
 |||||  
 Db 170 VKMDA 174

# RESULT 32

RSUA\_VIBVU

ID RSUA\_VIBVU STANDARD; PRT; 233 AA.  
 AC Q8D8X2;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70) (16S  
 DE pseudouridylate 516 synthase) (16S pseudouridine 516 synthase) (Uracil  
 DE hydrolyase).  
 GN RSUA OR VV12843.  
 OS Vibrio vulnificus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=672;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Responsible for synthesis of pseudouridine from  
 CC uracil-516 in 16S ribosomal RNA (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine  
 CC 5'-phosphate + H(2)O.  
 CC -!- SIMILARITY: Belongs to the pseudouridine synthase rsuA family.  
 CC -!- SIMILARITY: Contains 1 S4 RNA-binding domain.  
 CC -----  
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 CC -----  
 DR EMBL; AE016806; AA011180.1; -.  
 DR InterPro; IPR006145; PseudoU\_synth.  
 DR InterPro; IPR000748; Psi\_\_synth\_RSU.  
 DR InterPro; IPR002942; S4.  
 DR Pfam; PF00849; PseudoU\_synth\_2; 1.  
 DR Pfam; PF01479; S4; 1.  
 DR SMART; SM00363; S4; 1.  
 DR TIGRFAMs; TIGR00093; TIGR00093; 1.  
 DR PROSITE; PS01149; PSI\_RSU; 1.  
 DR PROSITE; PS50889; S4; 1.  
 KW rRNA processing; Lyase; RNA-binding; Complete proteome.  
 FT DOMAIN 1 67 S4 RNA-BINDING.  
 FT ACT\_SITE 101 101 BY SIMILARITY.  
 SQ SEQUENCE 233 AA; 26592 MW; 9B1A9249A80C8912 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 233;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKMD 5  
 |||||  
 Db 88 EVKMD 92

# RESULT 33

## CD8A MOUSE

ID CD8A\_MOUSE STANDARD; PRT; 247 AA.  
 AC P01731;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE T-cell surface glycoprotein CD8 alpha chain precursor (T-cell surface  
 DE glycoprotein LYT-2).  
 GN CD8A OR LYT2 OR LYT-2.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=85270477; PubMed=3927298;  
 RA Nakauchi H., Nolan G.P., Hsu C., Huang H.S., Kavathas P.,  
 RA Herzenberg L.A.;  
 RT "Molecular cloning of Lyt-2, a membrane glycoprotein marking a subset  
 RT of mouse T lymphocytes: molecular homology to its human counterpart,  
 RT Leu-2/T8, and to immunoglobulin variable regions.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5126-5130(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86079485; PubMed=3935316;  
 RA Zamoyska R., Vollmer A.C., Sizer K.C., Liaw C.W., Parnes J.R.;  
 RT "Two Lyt-2 polypeptides arise from a single gene by alternative  
 RT splicing patterns of mRNA.";  
 RL Cell 43:153-163(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87231009; PubMed=3495785;  
 RA Nakauchi H., Tagawa M., Nolan G.P., Herzenberg L.A.;  
 RT "Isolation and characterization of the gene for the murine T cell  
 RT differentiation antigen and immunoglobulin-related molecule, Lyt-2.";  
 RL Nucleic Acids Res. 15:4337-4347(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C.AKR;  
 RX MEDLINE=89006895; PubMed=3267233;  
 RA Youn H.J., Harriss J.V., Gottlieb P.D.;  
 RT "Nucleotide sequence analysis of the C.AKR Lyt-2a gene: structural  
 RT polymorphism in alleles encoding the Lyt-2.1 T-cell surface  
 RT alloantigen.";  
 RL Immunogenetics 28:345-352(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86252252; PubMed=3487583;  
 RA Liaw C.W., Zamoyska R., Parnes J.R.;  
 RT "Structure, sequence, and polymorphism of the Lyt-2 T cell  
 RT differentiation antigen gene.";  
 RL J. Immunol. 137:1037-1043(1986).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-152 IN COMPLEX WITH H-2KB.  
 RX MEDLINE=99021475; PubMed=9806638;  
 RA Kern P.S., Teng M.K., Smolyar A., Liu J.H., Liu J., Hussey R.E.,  
 RA Spoerl R., Chang H.-C., Reinherz E.L., Wang J.-H.;  
 RT "Structural basis of CD8 coreceptor function revealed by  
 RT crystallographic analysis of a murine CD8alphaalpha ectodomain  
 RT fragment in complex with H-2Kb.";  
 RL Immunity 9:519-530(1998).  
 CC -!- FUNCTION: Identifies cytotoxic/suppressor T-cells that interact  
 CC with MHC class I bearing targets. CD8 is thought to play a role in  
 CC the process of T-cell mediated killing. CD8 alpha chains binds to  
 CC class I MHC molecules alpha-3 domains.  
 CC -!- SUBUNIT: In general heterodimer of an alpha and a beta chain



```

CC      linked by two disulfide bonds. Can also form homodimers.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=1;
CC          Comment=A number of isoforms are produced. Alternative splicing
CC          involves excision of the transmembrane or cytoplasmic domains;
CC          Name=1;
CC          IsoId=P01731-1; Sequence=Displayed;
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M12825; AAA39476.1; -.
DR      EMBL; M16981; AAA39477.1; ALT_TERM.
DR      EMBL; M12052; AAA39478.1; -.
DR      EMBL; Y00157; CAA68352.2; -.
DR      EMBL; M22064; AAA39665.1; -.
DR      EMBL; M12977; AAA39475.1; -.
DR      EMBL; M12819; AAA39475.1; JOINED.
DR      EMBL; M12975; AAA39475.1; JOINED.
DR      EMBL; M12976; AAA39475.1; JOINED.
DR      PIR; A01998; RWMST2.
DR      PIR; A29523; A29523.
DR      PDB; 1BQH; 19-AUG-98.
DR      MGD; MGI:88346; Cd8a.
DR      GO; GO:0009986; C:cell surface; IDA.
DR      GO; GO:0042101; C:T-cell receptor complex; ISS.
DR      GO; GO:0015026; F:coreceptor activity; ISS.
DR      GO; GO:0042288; F:MHC class I protein binding; ISS.
DR      GO; GO:0005515; F:protein binding; ISS.
DR      GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
DR      GO; GO:0045065; P:cytotoxic T-cell differentiation; IMP.
DR      GO; GO:0006955; P:immune response; ISS.
DR      GO; GO:0042110; P:T-cell activation; ISS.
DR      GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003599; Ig.
DR      Pfam; PF00047; ig; 1.
DR      SMART; SM00409; IG; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin domain; Transmembrane; T-cell; Antigen; Glycoprotein;
KW      Immune response; Signal; Alternative splicing; 3D-structure.
FT      SIGNAL          1          27
FT      CHAIN           28         247      T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA
FT                                     CHAIN.
FT      DOMAIN          28         196      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        197         217      POTENTIAL.
FT      DOMAIN          218         247      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          28         139      IG-LIKE V-TYPE.
FT      DISULFID        53         129      POTENTIAL.
FT      CARBOHYD        69          69      N-LINKED (GLCNAC. . .).

```

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .).  
 FT VARIANT 105 105 M -> V (IN STRAIN C.AKR).  
 FT CONFLICT 81 81 MISSING (IN REF. 3).  
 SQ SEQUENCE 247 AA; 27456 MW; 22D0D78ECEC3EA04 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
 |||||  
 Db 40 KMDAE 44

# RESULT 34

## COX2\_METSE

ID COX2\_METSE STANDARD; PRT; 248 AA.  
 AC 047496;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).  
 GN COII.  
 OS Metridium senile (Brown sea anemone) (Frilled sea anemone).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Metridiidae; Metridium.  
 OX NCBI\_TaxID=6116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95055795; PubMed=7966369;  
 RA Pont-Kingdon G.A., Beagley C.T., Okimoto R., Wolstenholme D.R.;  
 RT "Mitochondrial DNA of the sea anemone, Metridium senile (Cnidaria):  
 RT prokaryote-like genes for tRNA(f-Met) and small-subunit ribosomal RNA,  
 RT and standard genetic code specificities for AGR and ATA codons."  
 RL J. Mol. Evol. 39:387-399(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White morph;  
 RA Beagley C.T., Okimoto R., Wolstenholme D.R.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Cytochrome c oxidase is the component of the respiratory  
 CC chain that catalyzes the reduction of oxygen to water. Subunits 1-  
 CC 3 form the functional core of the enzyme complex. Subunit 2  
 CC transfers the electrons from cytochrome c via its binuclear copper  
 CC A center to the bimetallic center of the catalytic subunit 1.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- COFACTOR: Copper A.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase subunit 2 family.  
 CC -----  
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CC -----

DR EMBL; S75445; AAB32498.1; -.  
DR EMBL; AF000023; AAC04639.1; -.  
DR PIR; T11893; T11893.  
DR InterPro; IPR001505; Copper\_CuA.  
DR InterPro; IPR008972; Cupredoxin.  
DR InterPro; IPR002429; Cyt\_c\_ox\_2.  
DR Pfam; PF00116; COX2; 1.  
DR Pfam; PF02790; COX2\_TM; 1.  
DR PRINTS; PR01166; CYCOXIDASEII.  
DR ProDom; PD000131; Copper\_CuA; 1.  
DR PROSITE; PS00078; COX2; 1.  
KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;  
KW Electron transport; Respiratory chain.  
FT DOMAIN 1 43 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
FT TRANSMEM 44 65 POTENTIAL.  
FT DOMAIN 66 79 MITOCHONDRIAL MATRIX (POTENTIAL).  
FT TRANSMEM 80 99 POTENTIAL.  
FT DOMAIN 100 248 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).  
FT METAL 180 180 COPPER A (PROBABLE).  
FT METAL 215 215 COPPER A (PROBABLE).  
FT METAL 219 219 COPPER A (PROBABLE).  
FT METAL 223 223 COPPER A (PROBABLE).  
SQ SEQUENCE 248 AA; 28294 MW; A14199E19D383D96 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 248;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VKMDA 6  
| | | | |  
Db 189 VKMDA 193

#### RESULT 35

##### T2S1\_STRFI

ID T2S1\_STRFI STANDARD; PRT; 269 AA.  
AC O52512;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Type II restriction enzyme SfiI (EC 3.1.21.4) (Endonuclease SfiI)  
DE (R.SfiI).  
GN SFIIR.  
OS Streptomyces fimbriatus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=68197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;  
RT "Characterization of the SfiI restriction and modification genes."  
RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Recognizes the double-stranded sequence GGCCNNNNNGGCC  
 CC and cleaves before N-9.  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
 CC specific double-stranded fragments with terminal 5'-phosphates.  
 CC -----  
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 CC -----  
 DR EMBL; AF039750; AAB95365.1; -.  
 DR REBASE; 1655; SfiI.  
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.  
 SQ SEQUENCE 269 AA; 31044 MW; 3C48499BAA5205EA CRC64;

Query Match 62.5%; Score 5; DB 1; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8  
 |||||  
 Db 119 MDAEF 123

#### RESULT 36

##### SACT\_BACSU

ID SACT\_BACSU STANDARD; PRT; 276 AA.  
 AC P26212;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE SacPA operon antiterminator.  
 GN SACT OR IPA-47D OR BSU38070.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90299824; PubMed=2163394;  
 RA Debarbouille M., Arnaud M., Fouet A., Klier A., Rapoport G.;  
 RT "The sact gene regulating the sacPA operon in Bacillus subtilis  
 RT shares strong homology with transcriptional antiterminators."  
 RL J. Bacteriol. 172:3966-3973(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=95020537; PubMed=7934828;  
 RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,  
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,  
 RA Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,  
 RA Rapoport G., Danchin A.;  
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97  
 RT kb region from 325 degrees to 333 degrees."  
 RL Mol. Microbiol. 10:371-384(1993).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT *subtilis*.";  
 RL Nature 390:249-256(1997).  
 CC -!- FUNCTION: MEDIATES POSITIVE REGULATION OF THE SACPA OPERON BY  
 CC FUNCTIONING AS AN ANTITERMINATOR FACTOR OF TRANSCRIPTION.  
 CC -!- PTM: PHOSPHORYLATED AND INACTIVATED BY SACP (EII-SCR) (PROBABLE).  
 CC -!- SIMILARITY: Belongs to the transcriptional antiterminator bglG  
 CC family.  
 CC -----  
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 CC -----  
 DR EMBL; J03006; AAA22726.1; ALT\_INIT.  
 DR EMBL; X73124; CAA51603.1; -.  
 DR EMBL; Z99123; CAB15833.1; -.  
 DR PIR; S39702; S39702.  
 DR HSSP; P15401; 1AUU.  
 DR SubtiList; BG10593; sacT.  
 DR InterPro; IPR001550; BglG\_antitermin.  
 DR InterPro; IPR004341; CAT\_RBD.

DR Pfam; PF03123; CAT\_RBD; 1.  
 DR Pfam; PF00874; PRD; 2.  
 DR PROSITE; PS00654; ANTITERMINATORS\_BGLG; 1.  
 KW Transcription regulation; Activator; RNA-binding; Phosphorylation;  
 KW Complete proteome.  
 FT VARIANT 96 96 D -> Y (IN SACT30 MUTANT).  
 SQ SEQUENCE 276 AA; 32074 MW; F1D63E4BC7CFBA03 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
 |||||  
 Db 161 KMDAE 165

# RESULT 37

## FLAL\_VIBPA

ID FLAL\_VIBPA STANDARD; PRT; 284 AA.  
 AC Q03473;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Lateral flagellin.  
 GN LAFA OR VPA1548.  
 OS Vibrio parahaemolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=670;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BB22;  
 RX MEDLINE=93273702; PubMed=8501040;  
 RA McCarter L.L., Wright M.E.;  
 RT "Identification of genes encoding components of the swarmer cell  
 RT flagellar motor and propeller and a sigma factor controlling  
 RT differentiation of Vibrio parahaemolyticus.";  
 RL J. Bacteriol. 175:3361-3371(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RIMD 2210633 / Serotype O3:K6;  
 RX MEDLINE=22508454; PubMed=12620739;  
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,  
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,  
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;  
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism  
 RT distinct from that of V. cholerae.";  
 RL Lancet 361:743-749(2003).  
 CC -!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO  
 CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA. ESSENTIAL FOR LATERAL  
 CC FLAGELLAR SYNTHESIS AND SWARMING MOTILITY.  
 CC -!- SUBUNIT: Homopolymer.  
 CC -!- SUBCELLULAR LOCATION: Flagellar.  
 CC -!- MISCELLANEOUS: V.PARAHAEMOLYTICUS POSSESSES TWO FLAGELLAR SYSTEMS:  
 CC A SINGLE POLAR FLAGELLUM PROPELS THE BACTERIUM IN LIQUID  
 CC (SWIMMING), WHILE MULTIPLE LATERAL (PERITRICHOUS) FLAGELLA MOVE



CC THE BACTERIUM OVER SURFACES (SWARMING). THE POLAR FLAGELLUM IS  
CC SYNTHESIZED CONSTITUTIVELY BUT LATERAL FLAGELLA ARE PRODUCED ONLY  
CC UNDER CONDITIONS IN WHICH THE POLAR FLAGELLUM IS NOT FUNCTIONAL.  
CC THE PERITRICHIOUS FLAGELLA ARE UNSHEATHED AND POWERED BY THE PROTON  
CC MOTIVE FORCE.

CC -!- SIMILARITY: Belongs to the bacterial flagellin family.

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CC -----

DR EMBL; L06176; AAA27529.1; -.

DR EMBL; U52957; AAB07350.1; -.

DR EMBL; AP005089; BAC62891.1; -.

DR PIR; A40590; A40590.

DR InterPro; IPR001029; Flagellin\_C.

DR InterPro; IPR001492; Flagellin\_N.

DR Pfam; PF00700; Flagellin\_C; 1.

DR Pfam; PF00669; Flagellin\_N; 1.

DR PRINTS; PR00207; FLAGELLIN.

KW Flagellum; Complete proteome.

FT CONFLICT 36 36 F -> Y (IN REF. 1).

FT CONFLICT 38 38 V -> I (IN REF. 1).

FT CONFLICT 245 245 D -> E (IN REF. 1).

SQ SEQUENCE 284 AA; 29702 MW; 5DDE3C09D26E6948 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 284;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MDAEF 8

|||||

Db 112 MDAEF 116

#### RESULT 38

##### VINT\_BPML5

ID VINT\_BPML5 STANDARD; PRT; 371 AA.

AC P22884;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Integrase.

GN 33 OR INT.

OS Mycobacteriophage L5.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;

OC L5-like viruses.

OX NCBI\_TaxID=31757;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93211282; PubMed=8459766;

RA Hatfull G.F., Sarkis G.J.;

RT "DNA sequence, structure and gene expression of mycobacteriophage L5:



RT a phage system for mycobacterial genetics.";  
 RL Mol. Microbiol. 7:395-405(1993).  
 RN [2]  
 RP SEQUENCE OF 28-371 FROM N.A.  
 RX MEDLINE=91195302; PubMed=1901654;  
 RA Lee M.H., Pascopella L., Jacobs W.R. Jr., Hatfull G.F.;  
 RT "Site-specific integration of mycobacteriophage L5: integration-  
 RT proficient vectors for Mycobacterium smegmatis, Mycobacterium  
 RT tuberculosis, and bacille Calmette-Guerin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3111-3115(1991).  
 CC -!- FUNCTION: INTEGRASE IS NECESSARY FOR INTEGRATION OF THE PHAGE INTO  
 CC THE HOST GENOME BY SITE-SPECIFIC RECOMBINATION.  
 CC -!- SIMILARITY: Belongs to the "phage" integrase family.  
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 CC -----  
 DR EMBL; Z18946; CAA79409.1; -.  
 DR EMBL; M65194; AAA32256.1; ALT\_INIT.  
 DR PIR; S30978; S30978.  
 DR InterPro; IPR002104; Phage\_integrase.  
 DR Pfam; PF00589; Phage\_integrase; 1.  
 KW DNA recombination; DNA integration.  
 FT ACT\_SITE 349 349 TRANSIENT COVALENT LINKAGE TO DNA DURING  
 FT STRAND CLEAVAGE AND REJOINING (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 371 AA; 41810 MW; D2D449CE83A15A13 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
 |||||  
 Db 39 KMDAE 43

# RESULT 39

K193\_HUMAN

ID K193\_HUMAN STANDARD; PRT; 414 AA.  
 AC Q12765; Q8IWD1;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Protein KIAA0193.  
 GN KIAA0193.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Bone marrow;  
 RX MEDLINE=96281124; PubMed=8724849;  
 RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;  
 RT "Prediction of the coding sequences of unidentified human genes. V.  
 RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by  
 RT analysis of cDNA clones from human cell line KG-1.";  
 RL DNA Res. 3:17-24(1996).  
 RN [2]  
 RP REVISIONS TO N-TERMINUS.  
 RC TISSUE=Brain;  
 RX MEDLINE=22158633; PubMed=12168954;  
 RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
 RT "Construction of expression-ready cDNA clones for KIAA genes: manual  
 RT curation of 330 KIAA cDNA clones.";  
 RL DNA Res. 9:99-106(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Bourne S., Wollam C., Fielder T.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -----  
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 CC -----  
 DR EMBL; D83777; BAA12106.2; ALT\_INIT.  
 DR EMBL; AC004912; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; AC007285; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; BC040492; AAH40492.1; -.  
 FT CONFLICT 298 298 P -> H (IN REF. 4).

SQ SEQUENCE 414 AA; 46382 MW; 1B14D1007AE6BEBE CRC64;

Query Match 62.5%; Score 5; DB 1; Length 414;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7

||||

Db 196 KMDAE 200

#### RESULT 40

DCDA\_ARCFU

ID DCDA\_ARCFU STANDARD; PRT; 419 AA.

AC O29458;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Diaminopimelate decarboxylase (EC 4.1.1.20) (DAP decarboxylase).

GN LYSA OR AF0800.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;

OC Archaeoglobaceae; Archaeoglobus.

OX NCBI\_TaxID=2234;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

RA Venter J.C.;

RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997).

CC -!- CATALYTIC ACTIVITY: Meso-2,6-diaminoheptanedioate = L-lysine + CO(2).

CC -!- COFACTOR: Pyridoxal phosphate.

CC -!- PATHWAY: Lysine biosynthesis; last step.

CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE DECARBOXYLASES.

CC -----  
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CC -----

DR EMBL; AE001049; AAB90438.1; -.  
 DR PIR; H69349; H69349.  
 DR TIGR; AF0800; -.  
 DR InterPro; IPR002986; DAP\_decrbxlase.  
 DR InterPro; IPR000183; Decarbxylse2.  
 DR InterPro; IPR009006; Racem\_decarbox\_C.  
 DR Pfam; PF02784; Orn\_Arg\_deC\_N; 1.  
 DR Pfam; PF00278; Orn\_DAP\_Arg\_deC; 1.  
 DR PRINTS; PR01179; ODADCRBXLASE.  
 DR TIGRFAMs; TIGR01048; lysA; 1.  
 DR PROSITE; PS00878; ODR\_DC\_2\_1; 1.  
 DR PROSITE; PS00879; ODR\_DC\_2\_2; 1.  
 KW Lysine biosynthesis; Lyase; Decarboxylase; Pyridoxal phosphate;  
 KW Complete proteome.  
 FT BINDING 56 56 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 419 AA; 45871 MW; 4EB7CB6BEE932047 CRC64;

Query Match 62.5%; Score 5; DB 1; Length 419;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KMDAE 7  
 |||||  
 Db 327 KMDAE 331

Search completed: March 26, 2004, 15:33:32  
 Job time : 41.5 secs